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OM nucleic - nucleic search, using bw model

Run on: December 24, 2005, 12:16:53 ; Search time 10.133 Seconds
(without alignments)
11494.348 Million cell updates/sec

Title: US-10-782-096-1
Perfect score: 2049
Sequence: 1 atgacatcataaataa.....atgacatcatatcaatcaa 2049

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:.*
1: gb_ba:.*
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14: gb_hcg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2049	100.0	2049	6	CQ868318	CQ868318 Sequence
2	2016	98.4	1986	6	CQ868320	CQ868320 Sequence
3	1986	96.9	1986	6	CQ868322	CQ868322 Sequence
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7	236	11.5	3504	6	BD133574	BD133574 Protein h
8	236	11.5	3680	6	BD133575	BD133575 Protein h
9	235.6	11.5	2003	6	AX543928	AX543928 Sequence
10	235.6	11.5	2010	6	CS130956	CS130956 Sequence
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14	235.6	11.5	3621	6	CS130946	CS130946 Sequence
15	235.6	11.5	3621	6	CS132867	CS132867 Sequence
16	235.6	11.5	3621	6	AX543924	AX543924 Sequence
17	235.6	11.5	4874	6	CS130962	CS130962 Sequence
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ALIGNMENTS

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DEFINITION Sequence 19 from Patent WO2004074462.
ACCESSION CQ868318
VERSION CQ868318.1 GI:51998364
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
AUTHORS Garozzi, N., Hargies, T., Koziel, M.G., Duck, N.B. and Carr, B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 19 02-SEP-2004;
Athenix Corporation (US)
FEATURES
source location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 2049; DB 6; Length 2049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS C0868322
DEFINITION Sequence 23 from Patent WO2004074462.
ACCESSION C0868322
VERSION C0868322.1 GI:51998368
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
AUTHORS Delta-endotoxin genes and methods for their use
TITLE Patent: WO 2004074462-A 23 02-SEP-2004;
JOURNAL Athenix Corporation (US)
FEATURES
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ORIGIN
Query Match 96.9%; Score 1986; DB 6; Length 1986;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
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KEYWORDS
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    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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REFERENCE
  1 (bases 1 to 3471)
  Narva,K.E. and Fu,J.
  Novel Coleopteran-Active Toxins from Bacillus thuringiensis
  Unpublished (1994)
  2 (bases 1 to 3471)
  Fietelson,J.S.
  Direct Submission
  Submitted (15-DEC-1993) Jerald S. Fietelson, Molecular Biology,
  Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121,
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  Best Local Similarity 50.5%; Pred. No. 1.1e-34;
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 DEFINITION Sequence 1 from patent US 5554534.
 ACCESSION 125971
 VERSION 125971.1 GI:1605841
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 3471)
 AUTHORS Michael, T. B., Narva, K. B. and Foncegrada, L.
 TITLE Bacillus thuringiensis toxins active against scarab pests
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 Best Local Similarity 50.5%; Pred. No. 1.1e-34;
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 VERSION AB089299.1 GI:22122187
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 SOURCE Bacillus thuringiensis serovar galleriae
 ORGANISM Bacillus thuringiensis serovar galleriae
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
 AUTHORS Amano, S., Yamashita, C., Iizuka, T., Takeuchi, K., Yamanaka, S.,
 Cerf, D. and Yamamoto, T.
 TITLE A strain of *Bacillus thuringiensis* subsp. *galleriae* containing a
 novel cry8 gene highly toxic to *Anomala cuprea* (Coleoptera:
 Scarabaeidae)
 JOURNAL Biol. Control 28, 191-196 (2003)
 REFERENCE 2 (bases 1 to 3435)
 AUTHORS Amano, S. and Yamamoto, T.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2002) Shin-ichiro Amano, Hokkaido University,
 Graduate school of Agriculture, N999, Sapporo, Hokkaido 060-8589,
 Japan (E-mail: sangaku@abs.agr.hokudai.ac.jp, Tel: 81-11-706-2423,
 Fax: 81-11-706-2423)

FEATURES
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Query Match 11.5%; Score 236; DB 1; length 3435;
 Best Local Similarly 55.9%; Pred. No. 3.6e-31;
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Db	169	TTTGGAAATCCGGAGACGTTTATTATAGTTCATCTACGAGTTTCAAACTGGAATGGCATTGTT	228
QY	253	GGGACTATACCTTTGGAAATTTAGGGGTCCCTTTGGCAATCAATCACTTTGGAAATATATGT	312
Db	229	GGTCAAGTACTGGGGGCTTTAGGGGTTCATATTTGCTGACAGATATGCTAGTTTTTAAATGT	288
QY	313	AGGCTAATAGGATATTTTATGGCAGGGGCT-----GATCCATTTGAAGCACTTATGGTT	366
Db	289	TTTATTTGTCGTTCAATTATATGGCCATCAAGTATCCGTGATGTATGGGAATATGATTATGAA	348
QY	367	CTTGTGGAAGCTTATTAAGAAAATATATGATCAGCTGTGAGAAAATGCTTTTATGA	426
Db	349	CAAGTGGAAAGTCTTAATTGATCAAAAATAACAGATTTCTGTATAGAAAACCGCGCTTCCA	408
QY	427	GAGCTAGAAGTTTATACGGGAATTAATGAGACTATTCAAATAGCTGACAGCATGCTGA	486
Db	409	GGACTACAGGATTAAGAGATGCGCTTAGACGTATATCGAATATCACTTAAGAAATGGGCTTG	468
QY	487	GTTAACAAAGATGATGACA--ATCGAGGGCACTAGTAACGACATATGCAATGTTGAT	543
Db	469	GAAATATGTAATGATATCAAGAGCTGAAAGTGTTGTGTGACCAATATATATGCTTTATAG	528
QY	544	AACCTTTTCGAAAAGAAATATGCCCAAAATTCAGAGAAAGAAAATTGAAATTTTATGTGA	603
Db	529	CTTGAATTTTGTGCTAAATCCCACTTTTGCAATATCTGACAGGAAGTACCAATTATTA	588
QY	604	CCAGTATATGACAAACCGCAAAATTTGCATTTAATTTATTAAGATGCTGATTAATTT	663
Db	589	TCACTGTATGACAAACGACGCAATTTACATTTGCTATTTATTAACGAGATGCTTCCATTTT	648
QY	664	GGAGCAACGTGGCAATTAAGTGATGATGAATTCGTGTAATATATATACACTACAGGA	723
Db	649	GGACACAGAGTGGGGAATTCACACACAGGAATAATTCACATTTTATATGATGCTGACGTGACA	708
QY	724	CTGATTAAGAAATTAATAGATCATTTGTATTAACATCTTAACACGAGGTTTAAATCAATTT	783
Db	709	CGTACCGCCCAATATCTCGAATTTATGTGTAAAGTGTAATACACTGGGCTTGATTAATTA	768
QY	784	AATCGCTCAAAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTTCTGTACAGATATGACATTA	843
Db	769	AAAGGTACGAATGCTGCAAGTTGGCTGAAGTATCACAATTCGGAAGGAATGACATTA	828
QY	844	ACAGTATTAAGATCTCGCAATATATTTCCAAACTATGATCCACGTAGGTATTCATTAGCA	903
Db	829	CTGTATTTAAGATTATAGTACGTTAATTTCCAAACTATGACACACGTACGTATTCATTCGAA	888

Qy	904	GTAAAAACGGAATTGACTAGGGAAGTTATACACATCCAGTAGGGATTACTCGGGTATTA	963
Db	889	ACAAAGCCCACTTACACGGGAAGTATACATCCAAATGATTTTAA	948
Qy	964	GAAGTGGAGGTAGA	979
Db	949	AGTGTGGATTTTGTGA	964

LOCUS	DEFINITION	BD133574	3504 bp	DNA	linear	PAT 18-SEP-2002
BD133574	Protein having insecticidal activity, DNA encoding the protein, and controlling agent and controlling method of noxious organisms.					

ACCESSION	BD133574
VERSION	BD133574.1
KEYWORDS	GI:23228519
SOURCE	JP 2002045186-A/1.
ORGANISM	<i>Bacillus thuringiensis</i> <i>Bacillus thuringiensis</i>

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 3504)	Asano, S., Yamana, S. and Takeuchi, K.	Protein having insecticidal activity, DNA encoding the protein, and controlling agent and controlling method of noxious organisms	Patent: JP 2002045186-A 1 12-FEB-2002;

FEATURES	Location/Qualifiers
SOURCE	1. .3504

ORIGIN

Query Match	11.5%	Score 236;	DB 6;	length 3504;
Best Local Similarity	55.9%	Pred. No. 3.5e-31;		
Matches 546;	Conservative 0;	Mismatches 400;	Indels 30;	Gaps 4.

Qy	13	AAAAATAAAATGAATGAAATGTTGGATGCTTACAGATCAACTCAATATGCTAAT	72
Db	10	AATATCAAAATGATATGAAATTCGTAGTCTTCATCATCTA---CTTCGTATCCGAT	66
Qy	73	TGTTATCCAAAGTATCACTAGCAAAAGATCCAAATGACTATGCCAAACGACATAT	132
Db	67	AATCTGTAGATGCCCTTTAGCAAAAGATCAAAACGACCATTTACAAAACATGAACAT	126
Qy	133	AAAGAATGGCTAAATATGTGATTCAAATACAAATTTATGGGATATTAAGACGTAAT	192
Db	127	AAAAATTATCTGAAATATGCTGAG-----GGAGGAATCCTGAATTA	168
Qy	193	TCTAGCCCTGAAGCTGCTTTAAGTACAGAGATCTGTTTTAAGCGGATTTAAACGTGTA	252
Db	169	TTTGGAAATCCGAGACGTTTATTAAGTTCACTACGGTTCAAACTGGAATGGCATTGTT	228
Qy	253	GGACATTACTTTGCAATTTAAGGGGTCCCTTTGGCAAGTCAATCATTTGGAAATATTAATG	312
Db	229	GGTCAGATCTAGGGGGCTTTAAGGGGTTCATTTCTGGACGATAGCTAGTTTTATATGT	288


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QY 313 AGGCTAATAGTATTTATTTATGGGCGGCGCT-----GATCCATTGGAAGCACTTATGTT 366
DB 289 TTGATATGTCGTCAATTTATGCGCATCAAGTACCGTGTATGTATGGAAATGATTTATGAAA 348
QY 367 CTGTTGGAAGAGCTTATTAAGAAAAGTATGATCAGCGTGTAAAGAAAATGCTTTTGA 426
DB 349 CAAGTGAAGATCTAATTTGATCAAAAATTAACAGATCTGTAAAGAAAACAGCGCTTGCA 408
QY 427 GAGCTAAGAGTTTACAGGGAATTTATGACTATATCAAACTAGACTGCAAGACATGGCTTA 486
DB 409 GGACTACAGAGATTAGAGATGCGTTAGACGTATATCAAGAAATCACTTAAGAAATGGCTG 468
QY 487 GTTAACAGAAATGATGACA---ATCGAGGGGCACTAGTAAAGCAAGTATGCAATTTGAT 543
DB 469 GAAATTCGTATATATACAAAGCTAGAGAGTGTGTGTGACCCAAATATATAGCTTTAGAG 528
QY 544 AACTTTTTCGAAAAGATATGCGCAAAATTCAGAGAAAAGAACTTTGAATTTTATGTTTA 603
DB 529 CTGATTTTGTGCTAAATATCCCATCTTTTGCAATATCTGACAGAGAAATACCATTTATA 588
QY 604 CCAGTATATGACAAAGCCGGAATTTGCAATTTATTTATTAAGAGATGCTGATTTATTT 663
DB 589 TCAGTATATGACAAAGAGCAAGAAATTTACATTTGCTATTTATTAAGAGATGCTTCATTTT 648
QY 664 GGAGCAAGTGGCAATTAAGGTATGATGAATTCGTGATATTTATATCAGACTACAAAGA 723
DB 649 GGAGCAAGTGGGAGATTCACACAGAGAAATTTCCACTTTTATATGATGCTCAGGTGACA 708
QY 724 CTGATTAAGAAATATTAAGATCATTTGTATTAACATTTCTATTAACAGAGGTTTAAATCA 783
DB 709 CGTACCGCCCAATATCTCGATTTATGTATGTAAGTGTATTAACATGCTGCTTATTAATTA 768
QY 784 AATCGCTCAAAATCTCAAGTTGGGTGAGCTTTATATAGTTTGTGTACAGATATGACTTTA 843
DB 769 AAGGATACAGATCTCGAAGTGTGCTGAGATATCAACCATTTCGAGAGAAATGACATTA 828
QY 844 ACAGTATTAATGATCTCGCAATATTTATTTCCAACTATGATCCAGTATGATTTCCATTAGA 903
DB 829 CTGCTATTAATTAATTAAGCTTATTTTCCAACTATGATCAGCTATGATTTCCATTAGA 888
QY 904 GTTAAAAACGAAATTAAGTAAAGTATTAATGATATCAGATCAGTATGAGTTTATCGGGTATTA 963
DB 889 ACAACGGCCCACTTACACGGGAAGTATATACGATCATATGATTTTACAGAGAAACA 948
QY 964 GAAAGTGGAGGTATGCA 979
DB 949 AGTGTGTGATTTTGTGA 964

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RESULT 8
BD133575 3690 bp DNA linear PAT 18-SEP-2002
LOCUS Protein having insecticidal activity, DNA encoding the protein, and
DEFINITION controlling agent and controlling method of noxious organisms.
ACCESSION BD133575
VERSION BD133575.1 GI:23228520
KEYWORDS JP 2002045186-A/2.
SOURCE JP 2002045186-A/2.
ORGANISM *Bacillus thuringiensis*
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 3690)
Amano, S., Yamana, S. and Takeuchi, K.
Protein having insecticidal activity, DNA encoding the protein, and
controlling agent and controlling method of noxious organisms
Patent: JP 2002045186-A 2 12-FEB-2002;
SDS BIOTECH KK
OS *Bacillus thuringiensis*
PN JP 2002045186-A/2
PD 12-FEB-2002
PF 03-AUG-2000 JP 200236140
PI SHINICHIRO ASANO, SATOSHI YAMANAKA, KATSUYOSHI TAKEUCHI PC

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FEATURES
source
location/Qualifiers
1..3690
/organism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/db_xref="taxon:1428"

ORIGIN
Query Match 11.5%; Score 236; DB 6; Length 3690;
Best Local Similarity 55.9%; Pred. No. 3,5e-31;
Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

QY 13 AAAAAATTAAGATTAATGAATGTTGATGCTTTACGAATCACTTAATATGCTTAAT 72
DB 196 AATATCAAAATGAATATGAATTTTATGATGCTTATCATCTA---CTTCTGATCCGAT 252
QY 73 TGTATTCAGAGTATCCATCGAAGAAAGATCCAAATGACTTTGCGAAACAGAACTAT 122
DB 253 AATTTGTTAGATACCTTTTGAAGAAAGATCAACGACCATTTATCAAAACATGAATAT 312
QY 133 AAGAAATGGCTAATATATGTTGATTCAAATATACAAATTTATGATATTAACAGCTAT 192
DB 313 AAGATATATCGAATGCTGAG-----GGAGGATTCGAAATTA 354
QY 193 TCTAGCCCTGAAGCTGTTTAAGTATGACAGATGCTGTTTAAACGGTATTAACAGTGA 252
DB 355 TTGGAATTCGAGAGAGTTTATTAAGTATCTACAGGTTCAACTGGAATTTGCAATGTT 414
QY 253 GGAATATATCTTTGCAATTTTGAAGGTCCTTTGGCAAGTAAATCATTTGGAATTAATAGT 312
DB 415 GTTCAAGTATCTGGGGCTTTTGAAGGGTTCATTTGCTGAGACAGATAGCTATTTTATAGT 474
QY 313 AGGCTAATAGTATTTATGAGGAGGCGCT-----GATCCATTGGAAGCACTTATGTT 366
DB 475 TTGATTTGCTGCTCAATTTATGAGCAATCAAGTACCGTATATGAGAAATGATTTAGAAA 534
QY 367 CTGTTGGAAGAGCTTATTAAGAAAGTATGATCAGGTGTAAAGAAAATGCTTTTGA 426
DB 535 CAAGTGAAGATCTAATTTGATCAAAAATTAACAGATTTCTGTAAAGAAAACAGCGCTTGCA 594
QY 427 GAGCTAAGAGTTTACAGGGAATTTATGACTATATCAAACTAGACTGCAAGACATGGCTTA 486
DB 595 GGACTACAGAGATTAGAGATGCGTTAGACGTATATCAGAAATCACTTAAGAAATGGCTG 654
QY 487 GTTAACAGAAATGATGACA---ATCGAGGGGCACTGTATACGAGTATGCAATTTGAT 543
DB 655 GAAATTCGTATATATCAAGAGCTAGAGTGTGTGTGACCCAAATATATAGCTTTAGAG 714
QY 544 AACTTTTTCGAAAAGATATGCGCAAAATTCAGAGAAAAGAACTTTGAATTTTATGTTTA 603
DB 715 CTGATTTTGTGCTAAATATCCCATCTTTTGCAATATCTGACAGAGAAATACCATTTATA 774
QY 604 CCAGTATATGACAAAGCCGGAATTTGCAATTTTATTTATTAAGAGATGCTGATTTATTT 663
DB 775 TCAGTATATGACAAAGAGCAAGAAATTTTCAATTTTATTTATTAAGAGATGCTTCATTTT 834
QY 664 GGAGCAAGTGGCAATTAAGGTATGATGAATTCGTGATATTTATATATCAGACTACAAAGA 723
DB 835 GGAGCAAGTGGGAGATTCACACAGAGAAATTTCCACTTTTATGATGCTCAGGTGACA 894
QY 724 CTGATTAAGAAATATTAAGATCATTTGTATTAACATTTCTATTAACAGAGGTTTAAATCAATTT 783

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Db 895 CGTACCGCCCAATCTCGATTATTTGTGTAAGTGATATACACTGGCTTAAATTA 954
Qy 784 AATCGCTCAAAATCTGAAGATTTGGTGAGCTTTAATAGTTTGTTCATACAGATATGACATTA 843
Db 955 AAGAGTACGAATCTGGAAGTTGGCTGGAATATCAACAATTCGAGAGAAATGACATTA 1014
Qy 844 ACAGTATTAGATCTCGCAATATTTTTCGAACTATGATCCAGTATGATTCATTAAGCA 903
Db 1015 CTGGTATTGATTTAGTAGGCTATTTCCAACTATGACACAGTATGATTCGAA 1074
Qy 904 GTAAAAACGGAATTGACTAGGAAGTTTATACAGATCCAGTATGAGTTTACTGGGATTA 963
Db 1075 ACAACGCCCAATTTACACGGGAAGTATACAGATCCAAATGATTTTACAGAGAAACA 1134
Qy 964 GAAAGTGAGATGAGA 979
Db 1135 AGTGTGGAATTTGTA 1150

RESULT 9
AX543928 2003 bp DNA linear PAT 23-NOV-2002
LOCUS Sequence 5 from Patent WO0234774.
DEFINITION AX543928
ACCESSION AX543928 GI:25277387
VERSION AX543928.1
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
AUTHORS
1 Abad,A.R., Duck,N.B., Feng,X., Flanagan,R.D., Kahn,T.W. and Sims,J.E.
TITLE
Gene encoding novel proteins with pesticidal activity against coleopterans
JOURNAL
Patent: WO 0234774-A 5 02-MAY-2002;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
source
1. 2003
Location/Qualifiers
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/db_xref="taxon:1428"
/note="(Truncated)
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1. .>2001
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/cramel_table=1
/protein_id="CAD57544.1"
/db_xref="GI:25277388"
/translation="MSPNNQVEYIIDATPSTSVSNDNRYPANSEPTNALQNDYKD
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NGSRARADYRNPREIILDSLPTQYMPSPRYPEVPLTYAMAAHLLIKDASIFG
EENKSTTTINNYIDRQMKLTAYSDHCVMETGAKLKAGTSAKQMDVNDQPREMT
LAVLDVALEPNYDTRTYPMETRAQLREVYDPLGAVNVSGISGYDAPSGVLES
SVLRPHVFDYITGLTVYQSRISISSARYRHWAGHOISYHRVSRSNLQOMGTION
LHSTSTPEFDNYDIKTLKDAVLIDIVYGVYIFPGMEVFPMVNOLNRTKLK
YNPVSKDIIASTDSELBLPPTSDQNPESVSHRLCHTISI PATGNTGLVPSMT
HRSADLNTIYSDKITQIIPAVKMDNLPPIPVYKGGHGTGDLQYNRSTGSYGLFL
ARGLAEKAGKTRVRLATADIVLHVADAIQMPKTMNPEEDLTSKTFKADAIT
TTLNATDSSIALKHNLGBDPNSTLSGIYVYDRLEFIPVDIYF"

ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 2003;
Best Local Similarity 56.5%; Pred. No. 5.1e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
Qy 13 AAAAAATAAATAATGAATGATGAGCTTTTACGAATCAACTTAATATGCTTAAT 72
Db 10 AATATCAAAATGAATATGAAATTAATATGATGAGCACTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAAAGTATCCATGCAAAAAGATTCACAAATGACTATGCAAAACGAACTAT 132

Db 67 GATTCTAACAGATACCTTTTGGAAATGAGCCAAACAATGCGCTACAAAATATGATTAAT 126
Qy 133 AAGAATGCTAAATATGTGTGATATTCAAATATACAAATTTATTTGGATATATACAGCTAT 192
Db 127 AAGATTTATTTAAATGATCTGGGGAAATGCTAGGAATACCTGGTTCA----- 177
Qy 193 TCTAGCCCTGAAGCTGCTTTAAGTATACGAGATGCTGTTTTAAACGGTATTAACAGTGA 252
Db 178 -----CTGAAGTACTTGTTAGCCGACAAAGATGACGTAAAGGCCCAATTTGATATAGTA 231
Qy 253 GGGACTATATCTTTCGAATTTAAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAATAGT 312
Db 232 GGTAAATTAATCTATCAGGTTTAAAGGGTCCCATTTGTTGGCCGATGATGATCTTTTACT 291
Qy 313 AGGCTAATAGATATTTTATGAGGAGGAGCTGA-----TCCATTTGAAGCACTTAATGTT 366
Db 292 CAAGTATGATATTTCTGTGGCTTCAAGGGAAGAAAGTCAATGGAATTTTATAGAA 351
Qy 367 CTGTTGAAAGCTTATTTAAGAAAGATATGATCAGCGTGTAAAGAAAATGCTCTTAGA 426
Db 352 CAAGTATGAAAGCTTATTAATCAAAAAATAGCAATATGCAAGAAATTAAGGCTTTTCG 411
Qy 427 GAGCTGAAGCTTTACAGGAATATGAGACTATATCAAACTAGACTGCAAGATGCTGA 486
Db 412 GAATTTGAAGGATTTAGTATATTTATCAATTTATCTAATGCGCTTGAAGAAATGGAA 471
Qy 487 GTTAACAAGAAATGATGACATCGAGGAGCACTAGT---AACGAGTATGCAATTTGAT 543
Db 472 GAAATTCGAATGCTTCAGAGAGCTTACAGAGATGTCGAAATGATTTGAATTCGAGAT 531
Qy 544 AACTTTTGGAAAAGATATGCCAAAATTCAGAGAAAGAACTTTGAATTTATTTGTTA 603
Db 532 AGTTTATTTACGCAATATATATGCGATCTTTAGAGTACAAAATTTGAAGTACCATTCCTT 591
Qy 604 CCAATATATGCAACAGCCGGAATTTGCAATTTATTTTATAGATGCTGATTAATTT 663
Db 592 ACTGATATGCAATGAGCAGCCCACTTCAATTTATCTGTATTAAGAGCGGTCATTTT 651
Qy 664 GGAGCAGATGCGCAATTAAGTGATGATGAATTCGTGATATTTATATACACTTACAGCAAGA 723
Db 652 GGAAGGAATGAGGAGATGTCACAACTATCTATTAATATACATATATATATGCTCAATGAA 711
Qy 724 CTGATTAAGAAATATTAAGATCTTGTATATACATTTCTATTAACAGAGCTTTAAATCAATTT 783
Db 712 CTTACTGCAAGAAATATCTGATCACTGTGTAAAGTGTATGAAACTGCTTTAGCAAAATTA 771
Qy 784 AATCGCTCAAAATGCTCAAGATTTGGGAGCTTTAATAGTTTGTACAGTATGACATTA 843
Db 772 AAGGCAAGAGCGCTTAACAAATGAGGTTGACTATTAACCAATTCGTAGAGAAATGACACTG 831
Qy 844 ACAGTATTAGATCTCGCAATATTTATTTCCAACTATGATCCAGTATGATTCATTAAGCA 903
Db 832 GCGGTTTGAATGATTTGTCATTTATTTCCAAATATGACACAGCAAGTATCCAAATGGA 891
Qy 904 GTAAAAACGGAATTGACTAGGAAGTTTATACAGATCCAGTAGG 947
Db 892 ACAGAAACGCAACTTAACAGGAAGATATATACAGATCCACTGGG 935

RESULT 10
CS130956 2010 bp DNA linear PAT 02-AUG-2005
LOCUS Sequence 11 from Patent WO2005066349.
DEFINITION CS130956
ACCESSION CS130956
VERSION CS130956.1 GI:71793192
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE
AUTHORS
1 Abad,A.

Matches	533;	Conservative	0;	Mismatches	384;	Indels	27;	Gaps	4;
Qy	13	AAAAATAAAAATGAATATGAAATGTTGATGCTTTACGATCAACTTAATATGCTAAT	72						
Db	10	AATATCAAAATGAATATGAAATTTATATGATGACACCTTCTA---CTTGTATCAAT	66						
Qy	73	TGTTATCCAAAGTATCCATGACGAAAAAGATCCCAATATGACTATGGGAAACAGAACTAT	132						
Db	67	GATTCTAACAGATACCTTTTGGGAATGAGCCCAACAAATGCGCTAACAAATATGATATAT	126						
Qy	133	AAAGATGGCTAAATATGTTGATGATTCCAATATACCAATTTATGATATTAAGACGATAT	192						
Db	127	AAAGATTTATTTAAAAATGTCTGGGGAAATGCTATGAAATACCTTGCTTA-----	177						
Qy	193	TCAGCCCTGAAGCTCTTTAAGTATGACGAGATGCTGTTTAAACGGTATTAACAGTAT	252						
Db	178	-----CTGAAATACCTTGTATGCGGACAAAGATGACAGCTAAGCCCAATGATATATAT	231						
Qy	253	GGGACTATATCTTTGCAATTTAAGGGTCCCTTTGGCAATCATCTTTGGAAATTAATAGT	312						
Db	232	GGTAAATTTACTATCAAGGTTTAAAGGGTCCCAATTTGTTGGCCGATGATGATCTTATACT	291						
Qy	313	AGGCTAATAGGTATTTTATGAGGAGGAGGCTGA-----TCCATTTGAAGCACTTATGTT	366						
Db	292	CAACTTATGATATTTCTGTGGCTTCAAGGGAAAAAGATCAATGGAAATTTTATATGAA	351						
Qy	367	CTTGTGAAAGCTTATTAAGAAATATATGATCAAGCTGTATTAAGAAAAATGCTCTTAA	426						
Db	352	CAAGTAAAGAACTATTTATCAAAAAATATGCAAAATATGCAAGAAATTAAGCGCTTTCG	411						
Qy	427	GAGCTTAAAGGTTTACAGGAAATTAATGACATATTCAAACTATGACTGCAAGATGGCTA	486						
Db	412	GATTATGAAGGATTAAGTATATATATCAATTTATATCTAACTCGCTTGAAGAAATGGAA	471						
Qy	487	GTTTAAACAAGATGATGACATGAGGAGGAGCTAGT---AAGCAGATGCAATTTGTTGAT	543						
Db	472	GAAATTCAAATGTTCTCAAGAGCTTACAGAGATGTCGAAATGATTTGAAATCTCGAT	531						
Qy	544	AACTTTTGGAAAAAGATATGCCCCAAATTCAGAGAAAGAACTTTGAAATTTATTTGTTA	603						
Db	532	AGTTTATTTTACGCAATATATATGATCTTTTATAGTGAACAAATTTTGAAGACATTCCT	591						
Qy	604	CCAGTATATGACACAGCCGGAATTTGATTTATTTTATTTAAGATGCTGATTAATTTT	663						
Db	592	ACTGTATATGCAATGACAGCAACCTTCACTTTACTGTTATTAAGACAGCGTCAATTTT	651						
Qy	664	GGAGCAGTGGCAATTAAGGTATGATGAATTCGGAATTAATATACAGACTACAAGGA	723						
Db	652	GGGAAAGAAATGGGAGTGTACACAACTACTATTTAATATATATATATATGATGCTCAAT	711						
Qy	724	CTGATTAGAAATATTAAGATCATTTGTATTAACATTTCTATTAACAGGGTTTAAATCAAT	783						
Db	712	CTTACTAGCAAAATATTTCTATCTATCTGTATTAAGTGTATTAAGAACTGTTTACGAAAT	771						
Qy	784	AATCGCTCAAGCTCAAGATTTGGGTAGCTTTAATATAGTTTGTACAGATATGACATTA	843						
Db	772	AAAGGACACAGCGCTTAAACATATGTTGACTATTAACCAATTCGTAGAGAAATGACACT	831						
Qy	844	AACGTTATGATTCGCCAATATTTTCCAACTATGATTCAGCTAGCTAGTATCCATAGCA	903						
Db	832	GGGGTTTATGATGTTGTGATTAATTTCCAAATTTATATGACACAGCACGTAACCAAT	891						
Qy	904	GTTAAAAACGAATTTGACTAGGAAATTTATACAGATCCAGTAGG	947						
Db	892	ACGAAAGCACAACTAACAGAGAAATATATACAGATCCACTGGG	935						

RESULT 12
BTU04365 3507 bp DNA linear BCT 27-AUG-1994
LOCUS Bacillus thuringiensis kumamotoensis P550C(b) CytIII
DEFINITION delta-endotoxin gene, partial cds.
ACCESSION U04365

VERSION	U04365.1	GI:436834
KEYWORDS	Bacillus thuringiensis	
SOURCE	Bacillus thuringiensis	
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.	
REFERENCE	1 (bases 1 to 3507)	
AUTHORS	Narva, K.E. and Fu, J.	
TITLE	Novel Coleopteran-Active Toxins from Bacillus thuringiensis	
JOURNAL	Unpublished (1994)	
REFERENCE	2 (bases 1 to 3507)	
AUTHORS	Fetelison, J.S.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-DEC-1993) Jerald S. Fetelison, Molecular Biology, Mycogen Corporation, 4980 Carrol Canyon Road, San Diego, CA 92121, USA	
FEATURES	Location/Qualifiers	
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ORIGIN	11.5%; Score 235.6; DB 1; Length 3507; Best Local Similarity 56.5%; Pred. No. 4,2e-31; Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;	
Qy	13	AAAAATAAAAATGAATATGAAATGTTGATGCTTTACGATCAACTTAATATGCTAAT
Db	10	AATATCAAAATGAATATGAAATTTATATGATGACACCTTCTAATC---TGATCAAT
Qy	73	TGTTATCCAAAGTATCCATGACGAAAAAGATCCCAATATGACTATGGGAAACAGAACTAT
Db	67	GATTCTAACAGATACCTTTTGGGAATGAGCCCAACAAATGCGCTAACAAATATGATATAT
Qy	133	AAAGATGGCTAAATATGTTGATGATTCCAATATTAACCAATTTATGATATTAAGACGATAT
Db	127	AAAGATTTATTTAAAAATGTCTGGGAAA-----TGTTAGTAATACCTT
Qy	193	TCAGCCCTGAAGCTCTTTAAGTATGACGAGATGCTGTTTAAACGGTATTAACAGTAT
Db	172	GGTTCACTCGAAGTATTTTCTAAGCGACAAAGATGCAAGTTAAGCCGCAATTTGATATATAT

OY	253	GGGACTATACCTTGCATTTTAGGGGCTCCCTTGGCAAGCATCATTTGGAAATTAATGT	312
Db	232	GGTAATTACTACACAGGTTTAGGGGCTTCATTGTGTGGCCGATGTGATCTTTATACT	291
OY	313	AGGCTAATAGGATATTTTAGGGC-----AGGGCTGATTCATTTGGAAGCCTTAGTGT	366
Db	292	CAACTTATTAATTAATCTGTGGCTTCAAACCAAAAGATGCATGGGAATTTTATGGA	351
OY	367	CTTGTGGAAGCTTATTTAAGAAAAGTATGATCAGCGTGTAAAGAAAATGCTTTAGA	426
Db	352	CAAGTAGAAGAACTATTAATCAAAAAATAGCAGATATGCAAGGAATTAAGCGCTTCG	411
OY	427	GAGCTAGAAGTTTACAGGAAATTATGAGCTATATCAAACTAGACTGACAGCATGCTA	486
Db	412	GAATTTGAAGGCTAGGGAAATTAATTAACAAATTAATCTTAACTGCGCTTGAAGATGGAA	471
OY	487	GTTAACAGAATGATGACATATCGAGGGCATAGT---AAGCAGATATGCATTTGTGAT	543
Db	472	GAATAATCCAAATGTTTCAAGAGCCTTAGAGATGTTCGAAATTCGATTTGAAATCCTGAT	531
OY	544	AACCTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTATGTGA	603
Db	532	AGTTATTTTAAGCATATATATGCAATCTTTTGAAGTACAAATTTGGAAGTACATTCCT	591
OY	604	CCAGTATATGCACAAGCCGCCGATTTGCATTTATTTATTAAGAGATGCTGATTTATTT	663
Db	592	ACAGTATATTAAGATGCGACAAACCTTAATTTACTTTTAAAGGAGCGCATCAATTTTT	651
OY	664	GGAGCAGTGGCATTAGTGATGATGAATTCGTGATTAATTAATCAGACTACAAGA	723
Db	652	GGAGAGAAATGGGGATGTGTTACAGCACTATTAATTAATCTACTAATATGCTAAATGAA	711
OY	724	CTGATTAAGAAATATAAGATCATTTGTATTAACATTCCTTAACAGGGTGTAAATCAATTT	783
Db	712	CTTACTGAGAAATATTTGCAGCACCTGTGTAAAGTGTATGAACCTGTTTAGCAAAATTA	771
OY	784	AATCGCTCAATGTCTCAAGATTTGGGTGAGCTTAAATAGGTTTCGTACAGATATGACATTA	843
Db	772	AAAGGCTCGAGGGCTTAACAATATGATTAAGCTTAATCAATTCCTGAGAAATGACATTTG	831
OY	844	ACAGTATTAAGATCTCGCAATATTAATTTCCAAACTATGATCCACGTATAGGTATTCATTAGA	903
Db	832	ACGGTGTTAGCGTGTTCGACTTATTTTCAAACTATGATAGCGGTACATTCACACTGCA	891
OY	904	GTAATAAACGGAATTGACTAGGGAATTTATATACAGATCCAGTAGG	947
Db	892	ACAAACAGCTCAGCTTACAAAGGAGATATATACAGATCCACTTGG	935

RESULT	13			
LOCUS	125972			
DEFINITION	I25972	3507 bp	DNA	linear
ACCESSION	Sequence 3 from patent US 5554534.			PAT 07-OCT-1996
VERSION	I25972.1	GI:1605842		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 3507)			
TITLE	Michaelis,T.E., Narva,K.E. and Foncerrada,L.			
JOURNAL	Bacillus thuringiensis toxins active against scarab pests			
FEATURES	Patent: US 5554534-A 3 10-SEP-1996;			
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Query Match	11.5%	Score 235.6;	DB 6;	length 3507;
Best Local Similarity	56.5%;	Pred. No. 4,2e-31;		
Matches 533; Conservative	0;	Mismatches 384;	Indels 27;	Gaps 4

OY	13	AAAAATAAAATGAATGAATGGAATGCTTTAGCAATCACTCAATATCTAAT	72
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Db	10	AATATCAAAATGAATATGAATTTATGATCGACCTTCAATC---TGATCAAT	66
OY	73	TGTTATCCAAAGTATCCATGACAAAGATCCACAAATGACTATGCGAAACGAATAT	132
Db	67	GATTCTAACAGATACCTTTTGGCAATGAGCAAAATGCGCTACAAATATGATTAAT	126
OY	133	AAAGAATGCTAATATGTGTGATTCAAATACAAATTTATGGTGAATATAGACGAT	192
Db	127	AAAGATTATTTTAAAAATGTCTGCGGAAA-----TGTTAGTAATACCTT	171
OY	193	TCTAGACCTGAAGCTGCTTTAAGTACAGATGCTGTTTTAACGGGTATTAACAGTGA	252
Db	172	GGTTCACCTGAGGATTTCTTAAGCAGACAGATGACTTTAAGCCGCAATTGATATGTA	231
OY	253	GGGACTATACCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGAAATTAATG	312
Db	232	GGTAAATTAATAACAGGTTTAGGGGTTTCATTTGTGGCGAATGATGACTTTAATCT	291
OY	313	AGGCTAATAGGATTTTATGCGC-----AGGCGCTGATCCATTTGAAAGCACTTATGTT	366
Db	292	CAACTATATGATATCTGTGTCCTTCAAAACAAAAGACTCAATGGAATTTTATGAA	351
OY	367	CTGTGTAAGACTTATTAAGAAAAGTATGATCAGCGTGAAGAAAATGCTCTTGA	426
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OY	427	GAGCTAGAAAGTTTACAGGGAATTAATGACTATATCAAACTAAGCTGCAAGATGCGTA	486
Db	412	GAATTTGAAGGGCTAGGGAATATTAACAAATATATCTTACCTGGCTGAAGATGGAAA	471
OY	487	GTTAAACAAGATGATGACATCGAAGGGCACTAGT--AACGAGTATGCAATGTGTGAT	543
Db	472	GAAATCCAAATGGTTCAMAGACCTTACGAATGTTCGAAATCGAATTTGAAATCCTGAT	531
OY	544	AACTTTTCGAAAAGATATATGCCAAATATCAAGAAAGAACTTTGAAATTTATGTTA	603
Db	532	AGTTTATTTACGCATATATATGCCATCTTTTGAAGTCAAAATTTTGAAGTACCATCTT	591
OY	604	CCAGTATATGCAACAGCCGCGAATTTGCATTTAAATTTTATTAAGATGCTGATTAATTT	663
Db	592	ACAGTATTAACAATGGGAGCAACCTACATTTACTTTATTAAGGAGCGCATCAATTTTT	651
OY	664	GGAGCACGTGGCAATTAGTGTGATGATGAATTTGCTGATTAATTATTCAGACTACAGGA	723
Db	652	GGAAGAAGATGGGAAATGTCTACACAGCATTTTATATACCTATTAATCGCAATGAA	711
OY	724	CTGATTTAGAAATTAAGATCATTTGATTAACATCTATTAACGAGGGTATTAATCAATTT	783
Db	712	CTTACTCGAATATTTCTGACCACTGTGTAAAGTGATGAACCTGGTTTAGCAAAATTA	771
OY	784	AATGCTCAAAATGCTCAAGATTTGGGTGAGCTTTATATAGTTTGTATACAGATATGACATTA	843
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OY	844	ACAGTATTAATCTTCGCAATTTATTTTCCAAACTATGATCCAAGTAGATATCCATTAGCA	903
Db	832	ACGGTGTAGACGTTGTTCATTTTTCAAACATATGATGAGCGGTACGATATCACCTGCA	891
OY	904	GTAATAACGAATTGACTAGGAAAGTTTATCAGATCCAGTAGG	947
Db	892	ACAAACGCTCAGTTTCAAGGGAAGTATATCAAGTCCACTTGG	935

RESULT 14	CS130946	3621 bp	DNA	1 ¹ linear	PAT 02-AUG-2005
LOCUS	CS130946				
DEFINITION	Sequence 1 from Patent WO2005066349.				
ACCESSION	CS130946				
VERSION	CS130946.1	GI:71793183			
KEYWORDS					
SOURCE	Bacillus thuringiensis				

ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Abad, A.
TITLE Genes encoding proteins with pesticidal activity
JOURNAL Patent: WO 2005066349-A 1 21-JUL-2005;
E.I. Du pont de nemours and company (US); Pioneer Hi-Bred International, Inc. (US)
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ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 3621;
Best Local Similarity 56.5%; Pred. No. 4,1e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAAATGTTGATGCTTTACGAATCAACTCTAATATGCTAAT 72
DB 10 AATTAATCAAAATGAATATGAAATTAATATGATGACACCTTCTA---CTTCTGATCCAAT 66

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QY 133 AAGAATGAGCTAATATGTTGATGCTCAATATACAAATTTATGATATATACAGATAT 192
DB 127 AAGATATATTTAAATATGCTGCGGGAATGCTAGTGAATACCTGTGTTA----- 177

QY 193 TCTAGCCCTGAAGCTGCTTTAAGTATGAGATGCTGTTTAAACGGATATTAACAGTAT 252
DB 178 -----CTGTAAGTACTTGTATAGCGGACAGATGACGCTAAGCCGCAATTTGATATATGTA 221

QY 253 GGAATATATCTTTGCAATTTTAAAGGGTCCCTTTGGCAAGTCAATCATTTTGAATATTAAGT 312
DB 232 GGTAAATTTATATCAGGTTTAAAGGGTCCCTTTGTTGGGCGGATAGATGATCTTTTATATCT 291

QY 313 AGGCTAATAGTATTTTATAGGCAAGGCGCTGA-----TCCATTTGAAGCACTTATAGT 366
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QY 367 CTTGTTGAAGAGCTTTTAAAGAAAGTATAGATCAGCGGTGAAGAAAAATGCTTTAGA 426
DB 352 CAAGTAGAAGAACTCAATTAATCAAAAAATAGAGATATGACAGATATAAGGGCTTTGCG 411

QY 427 GAGCTAGAAGGTTTACAGGAAATTAATAGACTATATCAACTAGACTGCAGCATGGCTA 486
DB 412 GAATTTGAAGGATTTAGTAAATTAATTAATCAATTTATCTTAATCTGCGTTGAAGAAATGGAA 471

QY 487 GTTAACMAAATGATGACAAATCGAGGACAGT---AACGAGTATGCAATGTTGAT 543
DB 472 GAAATCCAAATGTTTCAAGAGCCTTACGAGATGTGCAAAATCGAATTTGAAATCTCGAAT 531

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DB 532 AGTTAATTTAGCAATATATATGTCATCTTTTAAAGAGACAAATTTGAAGTACATTCCTT 591

QY 604 CCAGTATATGCACAAGCCCGCAATTTGATTAATTTTAAAGAGATGCTGATTTATTT 663
DB 592 ACTGTTATGCAATGAGCAGCAACTTCAATTTACTGTTTAAAGAGACCGCTCAATTTT 651

QY 664 GGAGCAAGTGGCAATTAAGTATGATGAATTCGTATATTAATATATAGACTTACAGGA 723
DB 652 GGAGAAAGATGGGAGATGTCACAACTACTATTAATATATATATGATGCTCAATGAA 711

QY 724 CTGATTAAGCAATATTAAGATCATTTATATACATTTATACAGAGGTTTAAATCAATT 783
DB 712 CTTACGCAAGATATTTCTATCATCTGTGTAAGGTGATAGAACTGTGTAGCAAAATTA 771

QY 784 AATCGCTCAATAGCTCAAGATTGGGAGCTTTAATAGGTTTCGTACAGATATGACATTA 843
DB 772 AAGGACACAGCGCTTAACAAATGGGTGACTATACCAATTCGTTAGAAATGACACTG 831

QY 844 ACAGTTATGATCTGCAATATTAATTTCCAACTATGATCAAGTAGATATCCATTAGCA 903
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QY 904 GTRAAAAACGAATGACTAGGGAATTTATACAGATCCAGTATG 947
DB 892 ACGMAAGCAACATCAAGGGAAGTATATACAGATCCACTGG 935

RESULT 15
CS132867
LOCUS CS132867 3621 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 5 from Patent WO2005063996.
ACCESSION CS132867
VERSION CS132867.1 GI:71791818
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Abad, A.
TITLE Plant activation of insect toxin
JOURNAL Patent: WO 2005063996-A 5 14-JUL-2005;
E.I. Du pont de nemours and company (US); Pioneer Hi-Bred International, Inc. (US)
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ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 3621;
Best Local Similarity 56.5%; Pred. No. 4,1e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAAATGTTGATGCTTTACGAATCAACTCTAATATGCTAAT 72
DB 10 AATTAATCAAAATGAATATGAAATTAATATGATGACACCTTCTA---CTTCTGATCCAAT 66

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OY 73 TGTATCCAAAGTATCCATAGCAAAAAGATCCAAATGACTATGCGAAAACAGACTAT 132
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Db 127 AAAGATTATTTAAATAATGTCGCGGAAATGCTAGTAATACCTGGTTCA----- 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 193 TCTAGCCCTGAGTGTCTTAAGTGTACGAGATGCTTTTAAACGGGTATTAACAGTGA 252
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Db 232 GGTAAATTACTATCAGGTTTAGGGGTCCCATTTGTTGGCGATATGAGTCTTATACT 291
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OY 313 AGGCTAATAGTATTTTATGGGCAAGGCTGA-----TCCATTTGAGCACTTATGTT 366
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OY 904 GTAAAAAGCAATTTAGTATAGGGAATTAACAGATCCAGTAGG 947
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Db 892 ACGAAAGCAACAACTAACAGGAAGTATATACAGATCCACTGGG 935
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Job time : 10141 secs

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XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
PI WPI; 2004-635574/61.
XX P-PSDB; ADR89408.
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptide, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
PS Claim 1; SEQ ID NO 19; 178bp; English.

CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxin of the invention, and methods for their production, are
CC specifically for the production of organisms with pesticide resistance,
CC specifically for the production of plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

SO Sequence 2049 BP; 688 A; 316 C; 403 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2049; DB 13; Length 2049;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATATATAAATAATGAATATGAATGTGGATGCTTACCAATCACTCT 60
DB 1 ATGAAATTCATATATAAATAATGAATATGAATGTGGATGCTTACCAATCACTCT 60
QY 61 AATATGCTAATTTGTTATCCAAAGGTATCACTAGCAAAAGATCCAAATGACTATGCGA 120
DB 61 AATATGCTAATTTGTTATCCAAAGGTATCACTAGCAAAAGATCCAAATGACTATGCGA 120
QY 121 AACACGAACCTATAAAGATGGCTTAATATGTGATTCAAATACAAATTTATTTGGTAT 180
DB 121 AACACGAACCTATAAAGATGGCTTAATATGTGATTCAAATACAAATTTATTTGGTAT 180
QY 181 ATAAGCAGTATCTAGCCCTGAAGCTGCTTAAGTACAGATGCTGTTTAAACGGGT 240
DB 181 ATAAGCAGTATCTAGCCCTGAAGCTGCTTAAGTACAGATGCTGTTTAAACGGGT 240
QY 241 ATTAACAGTATGGAATCTATATCTTGAATTTAGGGGTCCCTTTGGCAATCAATCTT 300
DB 241 ATTAACAGTATGGAATCTATATCTTGAATTTAGGGGTCCCTTTGGCAATCAATCTT 300
QY 301 GGAATATATAGTAGGCTTAATAGATTTTATGGCAGAGGCTGATCCATTTGAAGCACTT 360
DB 301 GGAATATATAGTAGGCTTAATAGATTTTATGGCAGAGGCTGATCCATTTGAAGCACTT 360
QY 361 ATGATCTTGTGTAAGAGCTTATTAAGAAAGTATAGATCAGCGGTGTAAGAAATGCT 420
DB 361 ATGATCTTGTGTAAGAGCTTATTAAGAAAGTATAGATCAGCGGTGTAAGAAATGCT 420
QY 421 CTTAAGAGCTAGAGGTTTACAGGGAATTAAGACTATATCAAACTAGACGCAAGCA 480
DB 421 CTTAAGAGCTAGAGGTTTACAGGGAATTAAGACTATATCAAACTAGACGCAAGCA 480
QY 481 TGGCTAGTTAAAGAAATGATGACATCGAGGCACTAGTAACGCGATGCAATTTGT 540
DB 481 TGGCTAGTTAAAGAAATGATGACATCGAGGCACTAGTAACGCGATGCAATTTGT 540
QY 541 GATTAATCTTTGAAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATTTG 600
DB 541 GATTAATCTTTGAAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATTTG 600

QY 601 TTACAGATATATGACAGAGCCGGAATTTGCAATTAATTTATTAAGAGATGCTGATAT 660
DB 601 TTACAGATATATGACAGAGCCGGAATTTGCAATTAATTTATTAAGAGATGCTGATAT 660
QY 661 TTGAGAGCAGAGGCAATTAAGGTATGATGAAATCGGATATATATATACAGATACAA 720
DB 661 TTGAGAGCAGAGGCAATTAAGGTATGATGAAATCGGATATATATATACAGATACAA 720
QY 721 GACATGATTAAGAAATATTAAGATTCATTTGATTAATCAATTTGATTAAGAGGTTTAAATCAA 780
DB 721 GACATGATTAAGAAATATTAAGATTCATTTGATTAATCAATTTGATTAAGAGGTTTAAATCAA 780
QY 781 TTTAATCGCTCAAAATGCTCAAGATTTGGTGAGCTTTAATATGCTTGTACATATGACA 840
DB 781 TTTAATCGCTCAAAATGCTCAAGATTTGGTGAGCTTTAATATGCTTGTACATATGACA 840
QY 841 TTACAGATATTAAGATTCGCAATATATTTCCAACTATGATCCAGTATGATCCATTA 900
DB 841 TTACAGATATTAAGATTCGCAATATATTTCCAACTATGATCCAGTATGATCCATTA 900
QY 901 GCAGTAAAAACGGAATTTGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTA 960
DB 901 GCAGTAAAAACGGAATTTGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTA 960
QY 961 TTGAAATGAGAGTATGACTTACCTTGATATCTTAATATATCAACCTTTACTGCT 1020
DB 961 TTGAAATGAGAGTATGACTTACCTTGATATCTTAATATATCAACCTTTACTGCT 1020
QY 1021 ATGGAATAATTAAGCAAGAGAGGCTCTTATATACAGTGGCTAATGATTTTGTAT 1080
DB 1021 ATGGAATAATTAAGCAAGAGAGGCTCTTATATACAGTGGCTAATGATTTTGTAT 1080
QY 1081 TATACAGAGCTCTAGATATATGCTGATGAGAAATATTTGGAGGGCATACATTA 1140
DB 1081 TATACAGAGCTCTAGATATATGCTGATGAGAAATATTTGGAGGGCATACATTA 1140
QY 1141 GTTGAATAATGAAATATGATGCTGAAATTAACCATTAATCTTGTAAATCTGATTT 1200
DB 1141 GTTGAATAATGAAATATGATGCTGAAATTAACCATTAATCTTGTAAATCTGATTT 1200
QY 1201 ACTGCTAATCAATTTTAAATTTGCGGAACCTTCTGTTTCAATATGATGATGCTGCT 1260
DB 1201 ACTGCTAATCAATTTTAAATTTGCGGAACCTTCTGTTTCAATATGATGATGCTGCT 1260
QY 1261 CGATATATTTTGAAGAGAAACAGAGGCTAAATTAATTAATTAAGTATGAGTCTCG 1320
DB 1261 CGATATATTTTGAAGAGAAACAGAGGCTAAATTAATTAATTAAGTATGAGTCTCG 1320
QY 1321 AGAGTATTTTATATATCAATTAATTAATTAATGATCTGATCTTTAAGATACGAAGTG 1380
DB 1321 AGAGTATTTTATATCAATTAATTAATTAATGATCTGATCTTTAAGATACGAAGTG 1380
QY 1381 CCGTCTAATCTTCCATCCGAACCTATATTAATGAGATTAACGAAAGGTAAGCCAAAG 1440
DB 1381 CCGTCTAATCTTCCATCCGAACCTATATTAATGAGATTAACGAAAGGTAAGCCAAAG 1440
QY 1441 CCAGAGCAGAGATTTTCCAGCATATATATCAAAATTTTGAATGACGCGCA 1500
DB 1441 CCAGAGCAGAGATTTTCCAGCATATATATCAAAATTTTGAATGACGCGCA 1500
QY 1501 AGTAGTTACAGGGGATTTGTTAGCTTTTAAAGCTTTGGGCAATACAGATATGAT 1560
DB 1501 AGTAGTTACAGGGGATTTGTTAGCTTTTAAAGCTTTGGGCAATACAGATATGAT 1560
QY 1561 CGTAATATCGTCTGAACAGATAAATTAATCAATATGATGACAGTAAAGGTTGGGGG 1620
DB 1561 CGTAATATCGTCTGAACAGATAAATTAATCAATATGATGACAGTAAAGGTTGGGGG 1620
QY 1621 GGGATATATGAGGTTTGTCAATCCAGAGCTTACGAGGGAATTTGGTAAAGTCAATGAT 1680
DB 1621 GGGATATATGAGGTTTGTCAATCCAGAGCTTACGAGGGAATTTGGTAAAGTCAATGAT 1680
QY 1681 AGTTGGCAATTCATTAAAGTTCAAGCAACAAAGCAAAAGCAAGTTATGTTGCTTTG 1740

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Db      1681 AGTTGGCATTCACCTTAAGTTCAAGCACCAAGAACAAAGTTATCGATTTCGTTTG 1740
Qy      1741 CGTTATGCTGTTAGTACCAATGGGAGATGCTATTTTGTAGAACACAGCGGAGATG 1800
Db      1741 CGTTATGCTGTTAGTACCAATGGGAGATGCTATTTTGTAGAACACAGCGGAGATG 1800
Qy      1801 CATATAGTTTCATTTTGTGATGCTCAATTCATCAGTGCATCAACACTCTTCTA 1860
Db      1801 CATATAGTTTCATTTTGTGATGCTCAATTCATCAGTGCATCAACACTCTTCTA 1860
Qy      1861 GAGAGGATTTTGGCTATATGATGTTCCAGATATTTTACACCATTAATAATCCCTTA 1920
Db      1861 GAGAGGATTTTGGCTATATGATGTTCCAGATATTTTACACCATTAATAATCCCTTA 1920
Qy      1921 ATAGAGATATGAGACAAAGCTTTGGTACCGCCGATAGCAAAATTTGAATTTATTCGA 1980
Db      1921 ATAGAGATATGAGACAAAGCTTTGGTACCGCCGATAGCAAAATTTGAATTTATTCGA 1980
Qy      1981 CTTAACACTTTTCCGATCAATCATCTTGAAGAAAAAGAGAACAGTAATGATCTATTT 2040
Db      1981 CTTAACACTTTTCCGATCAATCATCTTGAAGAAAAAGAGAACAGTAATGATCTATTT 2040
Qy      2041 ATCAATTAA 2049
Db      2041 ATCAATTAA 2049

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RESULT 2

ADR89409 standard; cDNA; 2016 BP.

AC ADR89409;

DT 18-NOV-2004 (first entry)

XX AXMI-009 alternative start site coding sequence.

XX 89: gene; delta-endotoxin; delta-endotoxin associated polypeptide;

KM expression cassette; transformation; transgenic; plant; bacteria;

KW lepidoptera; coleoptera; pest; pesticide; resistance;

XX pesticial activity.

OS Bacillus thuringiensis.

XX Key Location/Qualifiers

FT CDS 1..2016

FT /*tag= a

FT /product= "Alternative AXMI-009"

XX PN MO2004074462-A2.

XX PD 02-SEP-2004.

XX PF 20-FEB-2004; 2004MO-US005829.

XX PR 20-FEB-2003; 2003US-0448632P.

XX PR 20-FEB-2003; 2003US-0448633P.

XX PR 20-FEB-2003; 2003US-0448797P.

XX PR 20-FEB-2003; 2003US-0448806P.

XX PR 20-FEB-2003; 2003US-0448810P.

XX PR 20-FEB-2003; 2003US-0448812P.

XX PR 20-FEB-2004; 2004US-00782020.

XX PR 20-FEB-2004; 2004US-00782096.

XX PR 20-FEB-2004; 2004US-00782141.

XX PR 20-FEB-2004; 2004US-00782570.

XX PR 20-FEB-2004; 2004US-00783417.

XX PA (ATHE-) ATHENIX CORP.

XX PI Carozzi N, Hargis T, Koziel MG, Duck NB, Carr B;

XX XX

DR MPI, 2004-635574/61.
 XX P-PSDB; ADR89410.
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.

XX Claim 1; SEQ ID NO 21; 178bp; English.

CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.

XX Sequence 2016 BP; 668 A; 315 C; 400 G; 633 T; 0 U; 0 Other;

XX Query Match 98.4%; Score 2016; DB 13; Length 2016;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 2016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 ATGTTGATGCTTTACGATCAATCTAATATGCTAATTTTATCCAGATATCCACTA 93

Db 1 ATGTTGATGCTTTACGATCAATCTAATATGCTAATTTTATCCAGATATCCACTA 60

Qy 94 GCAAAAGATCCAAATGACTATGCGAAACAGAACTATTAAGAAATGATATGTGT 153

Db 61 GCAAAAGATCCAAATGACTATGCGAAACAGAACTATTAAGAAATGATATGTGT 120

Qy 154 GATTCAATATCAATTTATTTGATATATGAGACGATATCTAGCCCTGAAGTCTTTA 213

Db 121 GATTCAATATCAATTTATTTGATATATGAGACGATATCTAGCCCTGAAGTCTTTA 180

Qy 214 AGTGAAGAGATGCTGTTTACGAGGATTTACAGTGAAGACATATCTTGAATTTA 273

Db 181 AGTGAAGAGATGCTGTTTACGAGGATTTACAGTGAAGACATATCTTGAATTTA 240

Qy 274 GGGGTCCCTTGGCAAGTCAATCTTGAATATATGATGCTATATGATATTTATGG 333

Db 241 GGGGTCCCTTGGCAAGTCAATCTTGAATATATGATGCTATATGATATTTATGG 300

Qy 334 GCAGGCGCTGATCATTTGAAGCACTTATGCTTGTGAAGAGCTTATTAAGAAAGT 393

Db 301 GCAGGCGCTGATCATTTGAAGCACTTATGCTTGTGAAGAGCTTATTAAGAAAGT 360

Qy 394 ATAGATCAGGCTGTAAGAAATGCTCTTGAAGACTAGAAAGTTTACAGGAATTTATG 453

Db 361 ATAGATCAGGCTGTAAGAAATGCTCTTGAAGACTAGAAAGTTTACAGGAATTTATG 420

Qy 454 AGACTATATCAACTGATGCAAGCAATGCTTATTAAGAAATGATATGCAATCGGAGG 513

Db 421 AGACTATATCAACTGATGCAAGCAATGCTTATTAAGAAATGATATGCAATCGGAGG 480

Qy 514 GCATGTAAGCAAGTATGATGTTGATATCTTTTGAAGAAAGATATGCAAAATTC 573

Db 481 GCATGTAAGCAAGTATGATGTTGATATCTTTTGAAGAAAGATATGCAAAATTC 540

Qy 574 AAGAAAGAACTTTGAATTTTATTTATCAAGTATATGCAAGCCGGAATTTGCAT 633

Db 541 AAGAAAGAACTTTGAATTTTATTTATCAAGTATATGCAAGCCGGAATTTGCAT 600

Qy 634 TTAATTTTATTAAGATGCTGATTTATTTTGAAGCAATGGAATTAAGTATGATGA 693

Db 601 TTAATTTTATTAAGATGCTGATTTATTTTGAAGCAATGGAATTAAGTATGATGA 660

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QY 694 ATTGCGATTAATTATATCAGACTACAGAGCTGATTTAGAGAAATATAAGATCATTTGTATA 753
DB 661 ATTCGATATATATATCAGACTACAGAGCTGATTTAGAGAAATATAAGATCATTTGTATA 720
QY 754 ACATTTATATACAGAGGTTTAAATCAATTTAATCCGCTCAAAATCTCAAGTTGGGTAGC 813
DB 721 ACATTTATATACAGAGGTTTAAATCAATTTAATCCGCTCAAAATCTCAAGTTGGGTAGC 780
QY 814 TTTAATAGGTTTGTACAGATATGACATTTAAGATTTAGATCTCCCAATATATTTTCCA 873
DB 781 TTTAATAGGTTTGTACAGATATGACATTTAAGATTTAGATCTCCCAATATATTTTCCA 840
QY 874 AACTATGATCCAGTAGATATCCATTAGCAGTAAAAACGGAATTGACTAGGGAAGTTTAT 933
DB 841 AACTATGATCCAGTAGATATCCATTAGCAGTAAAAACGGAATTGACTAGGGAAGTTTAT 900
QY 934 ACAGATCCAGTAGAGGTTTACTGGGGTATTAGAAAGTGGAGTGGAGCTTAACCTTGTAT 993
DB 901 ACAGATCCAGTAGAGGTTTACTGGGGTATTAGAAAGTGGAGTGGAGCTTAACCTTGTAT 960
QY 994 AATCTTAATATATCAACCTTTAATGCTATGAAATATACAGACGAGCTCTCTTAT 1053
DB 961 AATCTTAATATATCAACCTTTAATGCTATGAAATATACAGACGAGCTCTCTTAT 1020
QY 1054 ACCACTTGGCTTAATGCTATTTTGTATATACAGAGCTCTAGATAATATGCTGATGTG 1113
DB 1021 ACCACTTGGCTTAATGCTATTTTGTATATACAGAGCTCTAGATAATATGCTGATGTG 1080
QY 1114 AGAAATATTTGGGAGAGGCTATACATTAAGTAAATAGAAATAGATGTTCTGAATATAC 1173
DB 1081 AGAAATATTTGGGAGAGGCTATACATTAAGTAAATAGAAATAGATGTTCTGAATATAC 1140
QY 1174 CATTAATTTGGTAAATCTGATTTATTTACTCTATTCAATATTTTATTTTCCGGAACCTT 1233
DB 1141 CATTAATTTGGTAAATCTGATTTATTTACTCTATTCAATATTTTATTTTCCGGAACCTT 1200
QY 1234 TCTGTTTTCAGTATGATGCTGCTGCTATATATTTAGAGAGAAACAGAGCTTAATAT 1293
DB 1201 TCTGTTTTCAGTATGATGCTGCTGCTATATATTTAGAGAGAAACAGAGCTTAATAT 1260
QY 1294 TATATTTCTATGATGATGAGAGTCTGAGAGTATTTTATATATCAATCAATATATATAT 1353
DB 1261 TATATTTCTATGATGAGAGTCTGAGAGTATTTTATATATCAATCAATATATATAT 1320
QY 1354 GTACCTGATCTTTAAGATGAGAGTCCGCTGCTAATCTTCATCCCAACTATATATATCA 1413
DB 1321 GTACCTGATCTTTAAGATGAGAGTCCGCTGCTAATCTTCATCCCAACTATATATCA 1380
QY 1414 GAATTTACAGAAAGATTAAGCCAAAGCCAAAGAGATTTTCAAGCATTATATCT 1473
DB 1381 GAATTTACAGAAAGATTAAGCCAAAGCCAAAGAGATTTTCAAGCATTATATCT 1440
QY 1474 TATATTTCAAAATTTTATGATGACGCGCAAGTATGTTGAGTCTTTTAAAG 1533
DB 1441 TATATTTCAAAATTTTATGATGACGCGCAAGTATGTTGAGTCTTTTAAAG 1500
QY 1534 TTTGTTGGGACATATCCAGTATGATCGTATATATCGTTTGAACCAATATAATTAATCT 1593
DB 1501 TTTGTTGGGACATATCCAGTATGATCGTATATATCGTTTGAACCAATATAATTAATCT 1560
QY 1594 CAAATGATGCAATTAAGGTTTGGGGGGGGAATATCGGTTTGTCAATCCAGAGACTTACT 1653
DB 1561 CAAATGATGCAATTAAGGTTTGGGGGGGGAATATCGGTTTGTCAATCCAGAGACTTACT 1620
QY 1654 GGGGGGAATTTGGTAAAGTCAAGTATAGTTGGCATTTCACTTAAAGTTCAAGACACACAA 1713
DB 1621 GGGGGGAATTTGGTAAAGTCAAGTATAGTTGGCATTTCACTTAAAGTTCAAGACACACAA 1680
QY 1714 AGACAAACAAGTATATGATGTTGCGTTAGCTGTTTGTATTTCCATCGGAGAGTGC 1773
DB 1681 AGACAAACAAGTATATGATGTTGCGTTAGCTGTTTGTATTTCCATCGGAGAGTGC 1740

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QY 1774 ATTTTGTATGAACACAGCGGCGAGTACTATATAGTTTCAATTTTGTATGCTCAATTCA 1833
DB 1741 ATTTTGTATGAACACAGCGGCGAGTACTATATAGTTTCAATTTTGTATGCTCAATTCA 1800
QY 1834 TCAGGTCGTCCATCAACAACCTCTTCAGAGAGTATTTTCCGCTATATGATGTTCCAGGT 1893
DB 1801 TCAGGTCGTCCATCAACAACCTCTTCAGAGAGTATTTTCCGCTATATGATGTTCCAGGT 1860
QY 1894 ATTTTACACATCAATTAATCCCTTAATATAGATATAGAACAAAGCTTTGTACCCAC 1953
DB 1861 ATTTTACACATCAATTAATCCCTTAATATAGATATAGAACAAAGCTTTGTACCCAC 1920
QY 1954 GCGATAGACAAATTTGAATTTATTCACCTTAACACCTTTCCGAATCAATTAAGAAAA 2013
DB 1921 GCGATAGACAAATTTGAATTTATTCACCTTAACACCTTTCCGAATCAATTAAGAAAA 1980
QY 2014 AGGAAACAGAGTAATATGATCAATTTATCAATTA 2049
DB 1981 AGGAAACAGAGTAATATGATCAATTTATCAATTTAA 2016

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RESULT 3

ADR89411

ID ADR89411 standard; cDNA; 1986 BP.

XX ADR89411;

DT 18-NOV-2004 (first entry)

XX

DE AXMI-009 alternative start site coding sequence #2.

KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.

XX

OS *Bacillus thuringiensis*.

XX

FH Key Location/Qualifiers

FT CDS

FT 1..1986
 FT /tag= a
 FT /product= "Alternative AXMI-009 #2"

FT

PN WO200407462-A2.

XX

PN WO200407462-A2.

XX

PN 02-SEP-2004.

PD

PF 20-FEB-2004; 2004WO-US005829.

XX

PF 20-FEB-2003; 2003US-0448632P.

XX

PR 20-FEB-2003; 2003US-0448633P.

XX

PR 20-FEB-2003; 2003US-0448797P.

XX

PR 20-FEB-2003; 2003US-0448806P.

XX

PR 20-FEB-2003; 2003US-0448810P.

XX

PR 20-FEB-2003; 2003US-0448812P.

XX

PR 19-FEB-2004; 2004US-00781979.

XX

PR 19-FEB-2004; 2004US-00782020.

XX

PR 19-FEB-2004; 2004US-00782096.

XX

PR 19-FEB-2004; 2004US-00782141.

XX

PR 19-FEB-2004; 2004US-00782570.

XX

PR 19-FEB-2004; 2004US-00783417.

XX

XX (ATHE-) ATHENIX CORP.

XX

XX Carozzi N, Hargis T, Koziel MG, Duck NB, Carr B;

XX

XX WPI; 2004-635574/61.

XX

XX P-PSDB; ADR89412.

XX

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.

XX

PS Claim 1, SEQ ID NO 23, 178bp, English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. CC The nucleic acid sequences of the invention are useful in DNA constructs CC or expression cassettes for transformation and expression in plants and CC bacteria. The nucleic acids and corresponding polypeptides are useful for CC killing lepidopteran or coleopteran pests. Compositions containing the CC delta-endotoxins of the invention, and methods for their production, are CC useful for the production of organisms with pesticide resistance, CC specifically bacteria and plants. These organisms are useful for CC generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the CC presence of delta-endotoxin or delta-endotoxin-associated proteins or CC nucleic acids in products or organisms.

XX Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other;

Query Match 96.9%; Score 1986; DB 13; Length 1986;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 ATGCTAATTTGTTATCCAAAGTATCCACTAGCAAAAGATCCCAAAATGATGCGAATC 123
DB 1 ATGCTAATTTGTTATCCAAAGTATCCACTAGCAAAAGATCCCAAAATGATGCGAATC 60
QY 124 ACCAATATTAAGAAAGGCTTAATATGATGATCAATACAAATTTATGATGATATA 183
DB 61 ACCAATATTAAGAAAGGCTTAATATGATGATCAATACAAATTTATGATGATATA 120
QY 184 AGCAGCTATTTCTAGCCCTGGAAGCTGTTAAGTACAGATGCTGTTTAAACGGATAT 243
DB 121 AGCAGCTATTTCTAGCCCTGGAAGCTGTTAAGTACAGATGCTGTTTAAACGGATAT 180
QY 244 AACAGCTAGGAGCTATATCTTTGAAATTAAGGGTCCCTTTGGCAAGTCAATCATTTGA 303
DB 181 AACAGCTAGGAGCTATATCTTTGAAATTAAGGGTCCCTTTGGCAAGTCAATCATTTGA 240
QY 304 ATAATAGTATGAGCTTAATAGGATTTTATGGGCGGGGCTATCCATTTGAAAGCATTA 363
DB 241 ATAATAGTATGAGCTTAATAGGATTTTATGGGCGGGGCTATCCATTTGAAAGCATTA 300
QY 364 GTTCTTGTTGAAGCTTATTAAGAAAGTATAGATCAGCGTGAAGAAAATGCTCTT 423
DB 301 GTTCTTGTTGAAGCTTATTAAGAAAGTATAGATCAGCGTGAAGAAAATGCTCTT 360
QY 424 AGAAGCTAGAAAGTTTACAGGGAATTAAGACTATATCAAACTAGACTGCAAGCATGG 483
DB 361 AGAAGCTAGAAAGTTTACAGGGAATTAAGACTATATCAAACTAGACTGCAAGCATGG 420
QY 484 CTAGTTTAAACAAGATGATGACAAATCGGAGGCACTATTAACGCGATATGCAATTTGAT 543
DB 421 CTAGTTTAAACAAGATGATGACAAATCGGAGGCACTATTAACGCGATATGCAATTTGAT 480
QY 544 AACCTTTTCAAAAAGATATGCAAAATTCAGAGAAAGAACTTGAATTTTATTTATGTTA 603
DB 481 AACCTTTTCAAAAAGATATGCAAAATTCAGAGAAAGAACTTGAATTTTATTTATGTTA 540
QY 604 CCAATATATGACAAAGCCGGAATTTGCAATTTTATTAAGAGATGCTGATTTATTT 663
DB 541 CCAATATATGACAAAGCCGGAATTTGCAATTTTATTAAGAGATGCTGATTTATTT 600
QY 664 GGAGCAAGTGGCAATTAAGTATGATGAAATTCGTATTAATTAATCAATCAAGAGA 723
DB 601 GGAGCAAGTGGCAATTAAGTATGATGAAATTCGTATTAATTAATCAATCAAGAGA 660
QY 724 CTGATTTAGAAATTAAGATCATTTATTAACATTTCTATAACGAGGTTTAAATCAATTT 783
DB 661 CTGATTTAGAAATTAAGATCATTTATTAACATTTCTATAACGAGGTTTAAATCAATTT 720
QY 784 AATGCTCAAAATGCTCAAGATGAGGCTTTAATAGTTTGTGATCAGATATGACATTA 843

DB 721 AATGCTCAAAATGCTCAAGATGAGGCTTTAATAGTTTGTGATCAGATATGACATTA 780
QY 844 ACAATATTAATCTCGCAATATTTATTTCCAAACTATGATCCAGTAGATATCCATTAGCA 903
DB 781 ACAATATTAATCTCGCAATATTTATTTCCAAACTATGATCCAGTAGATATCCATTAGCA 840
QY 904 GTAAAAACGAAATTTGACTAGGAAAGTTTATACAGATCCAGTAGGTTTACTGGGGTATTA 963
DB 841 GTAAAAACGAAATTTGACTAGGAAAGTTTATACAGATCCAGTAGGTTTACTGGGGTATTA 900
QY 964 GAAAGTGGAGTGGAGCTTACCCCTGGTATATCCCTTAATCAACCTTACGCTATG 1023
DB 901 GAAAGTGGAGTGGAGCTTACCCCTGGTATATCCCTTAATCAACCTTACGCTATG 960
QY 1024 GAAATATACCAAGACAGACGCTCTTCTTATACACTTGGCTTATCGTATTTTGTATAT 1083
DB 961 GAAATATACCAAGACAGACGCTCTTCTTATACACTTGGCTTATCGTATTTTGTATAT 1020
QY 1084 ACAAGACTAGGATTAATGCTGATGAGAAATTTTGGAGGGCATTAATAGTT 1143
DB 1021 ACAAGACTAGGATTAATGCTGATGAGAAATTTTGGAGGGCATTAATAGTT 1080
QY 1144 GAAATNGGAATGATGTTGTAATTAACCATTAACCTTGTAAACTGATTTCTATACT 1203
DB 1081 GAAATNGGAATGATGTTGTAATTAACCATTAACCTTGTAAACTGATTTCTATACT 1140
QY 1204 CCTATTCATATTTTAAATTTGCGAAGCTTCTGTTTCAGTATAGTCACTTGCCTGT 1263
DB 1141 CCTATTCATATTTTAAATTTGCGAAGCTTCTGTTTCAGTATAGTCACTTGCCTGT 1200
QY 1264 ATATATTTAGAGAAACAGAGGCTAATTAATTAATTAATTAATTAATTAATTAATTA 1323
DB 1201 ATATATTTAGAGAAACAGAGGCTAATTAATTAATTAATTAATTAATTAATTAATTA 1260
QY 1324 GTATTTTAAATACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1383
DB 1261 GTATTTTAAATACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
QY 1384 GCTATCTTCATCCCAACTATATATGAGATTAACAGAAAGATAACCAAGACA 1443
DB 1321 GCTATCTTCATCCCAACTATATATGAGATTAACAGAAAGATAACCAAGACA 1380
QY 1444 AACGAGAGATTTACGCCATATATATCTTATATATCAAAATTTTGAATGACGCGCAAGT 1503
DB 1381 AACGAGAGATTTACGCCATATATATCTTATATATCAAAATTTTGAATGACGCGCAAGT 1440
QY 1504 AGTTCAAGCGGATTTGTTAGTCTTTTAAAGTTGGTTGGGCAATACAGATATGATCGT 1563
DB 1441 AGTTCAAGCGGATTTGTTAGTCTTTTAAAGTTGGTTGGGCAATACAGATATGATCGT 1500
QY 1564 AATATTCGTTGTAACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1623
DB 1501 AATATTCGTTGTAACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
QY 1624 AATATTCGTTGTTGTAACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1683
DB 1561 AATATTCGTTGTTGTAACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1620
QY 1684 TGGCATTCATTAAGTTTCAAGACCAACAAGCAAAACAAAGTTATGATGCTTGGCT 1743
DB 1621 TGGCATTCATTAAGTTTCAAGACCAACAAGCAAAACAAAGTTATGATGCTTGGCT 1680
QY 1744 TATGCTGTTTATGTTACCAATGGGGATGCTAATTTTGTAGAACACAGCGGCAATGATCAT 1803
DB 1681 TATGCTGTTTATGTTACCAATGGGGATGCTAATTTTGTAGAACACAGCGGCAATGATCAT 1740
QY 1804 ATAGTTTCAATTTTGAATGCTCAAAATTCATCAGTGTGTCATCAAAACCTCTTCAAG 1863
DB 1741 ATAGTTTCAATTTTGAATGCTCAAAATTCATCAGTGTGTCATCAAAACCTCTTCAAG 1800
QY 1864 AGTGAATTTTGGCTATATGATGTTCCAGGATTTTATACACATCAATTAATCCCTTAATA 1923
DB 1801 AGTGAATTTTGGCTATATGATGTTCCAGGATTTTATACACATCAATTAATCCCTTAATA 1860


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Db 1126 ACCCTAAATATCGTAGAACAGCGATTCCAGCCGTAAACACAGCTAATACGGTCGA 1185
Qy 1195 TCAATTAATCTCTATTCATATTTTAAATTTGGCAACCTTCTGTTTCAGATTTGACTCA 1254
Db 1186 ATCACTTCAGAAAAGAAATTCATTTGCACTTGAGAGATAGGAGATTTTGAATTTAATTC 1245
Qy 1255 CTGCTCGTATATTTATTTAGAGAGAAACAGAGGCTAATAATATTAATTAAGTATGATGA 1314
Db 1246 ACTGTGGCAA---ACCTAGCTAATTAATACCAAAAGGCATATGTGTGCGGGATCTTGG 1302
Qy 1315 GTCTCGAGAGTTATTTTAAATACATCAATATTAATAATGATGATCTTTAAGATAC 1374
Db 1303 TTCATATGTGTAATAAAGGGAGACCTCATCAACACAGCTATTATTAATTCAAAAACAT 1362
Qy 1375 GAAGTCCCTGCTAATCTTCCATCCCAACATATATTAACAATTAACAGAAAGATTAAG 1434
Db 1363 ACAGCTCTCCAGAGGTGTACACAGTTTATGAATCAAGTATGAATTAAGTCTAGATGA 1422
Qy 1435 CCAAGACCAAAACGAGAGATTTCAAGCATAGATTAATCTTATATATCAAAATTTGATGA 1494
Db 1423 ACTGTACCGTAGCTGAAGAACTATAGTCATAGATTAATCTCAATTAATCTCCATCTTTC 1482
Qy 1495 CGGCGAAGTATGATCAAGCGGTATGTTAGTCTTTTAAAGTTGGTGGACATACCAAGT 1554
Db 1483 TCTAAATAATGGAGTGATCTATGGAAGTTCCCTGATTTGTTTGGACACATACAGT 1542
Qy 1555 ATGATATCTATATATGCTCTTGAACAGATTAATTAATTAATTAATGATGATGAAGT 1614
Db 1543 GCGGATTTAAATATATACAAATATATTCAGATTAATTAATCACTCAAAATTCAGCGGTAAAGGA 1602
Qy 1615 TGGGGGGGGAATATCGGGTTTGTATCCAGACCTACTGG 1655
Db 1603 GACATGTATATCTAAGGGGTTCCGTATGATCAAGGATCTGG 1643

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RESULT 5

AAQ27167
ID AAQ27167 standard; DNA; 3471 BP.

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XX AC AAQ27167,
XX DT 25-MAR-2003 (revised)
XX DT 27-JAN-1993 (first entry)
XX DE Delta-endotoxin gene.
XX KM B.t. PS50C; Colorado potato beetle; Leptinotarsa decemlineata;
XX KM Pseudomonas; expression vector; ss.
XX OS Bacillus thuringiensis.
XX PN EP498537-A2.
XX PD 12-AUG-1992.
XX PF 16-JAN-1992; 92BP-00300366.
XX PR 16-JAN-1991; 91US-00642112.
XX PA (MYCO ) MYCOGEN CORP.
XX PI Fonceerrada L, Sick AJ, Payne JM;
XX DR WPI; 1992-270497/33.
XX DR P-PSDB; AAR25997.
XX PT New insecticidal Bacillus thuringiensis strain NRRL B-18746 - and toxin,
XX PT DNA encoding it, vectors and transformed cells, effective against
XX PT Coleoptera.
XX PS Claim 8; Page 9-11; 16pp; English.
XX

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CC The sequence given encodes an approx. 130 kD protein known as Bacillus
CC thuringiensis PS50C (B.t. PS50C). This novel delta-endotoxin has been
CC shown to be active against the Colorado potato beetle (Leptinotarsa
CC decemlineata). This toxin gene can be transformed into suitable hosts
CC such as Pseudomonas, which can then be applied to the environment of
CC coleopteran insects, where they will proliferate and be ingested by the
CC insects. This sequence can be inserted into an expression vector which
CC contains a promoter/operator region, a ribosome binding site,
CC polyadenylation signals, etc. This will allow transcription and
CC translation of the cells in the appropriate host. (Updated on 25-MAR-2003
CC to correct EN field.)

XX Sequence 3471 BP; 1200 A; 567 C; 751 G; 953 T; 0 U; 0 Other;

Qy Query Match 12.5%; Score 256.2; DB 2; Length 3471;
Best Local Similarity 50.5%; Pred. No. 2.9e-49;
Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

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Qy 13 AAAAAATAAATGAAATATGAAATGTTGATGCTTTAGCAATCACTTAATATGCTTAAT 72
Db 10 AATTAATCAAAATGAATATGAAATTTATAGATGCGACACCTTCTATC---TGATCCAGT 66
Qy 73 TGTATTCAAAGTATCCACTAGCAAAAAGATCCCAAATGACTATGGGAAACAGAACTAT 132
Db 67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAACAGATGCGTTACAAATATGAATATAT 126
Qy 133 AAGAAATGGCTAATATATGATGATGATGCAATATACAAATTTATGGTATATTAACAGATAT 192
Db 127 AAGATATATCTGAAATATGCTGGG-----GAGAGAAATCTGAAATTA 168
Qy 193 TCTAGCCCTGAAAGCTCTTTAAGTATACAGATGCTGTTTAAACGGATATTAACAGTGA 252
Db 169 TTGGAAATCCGAGAGCGTTTATTAATGATCAACAGATTAATCGGAATATGCAATGTT 228
Qy 253 GCGACTATATCTTCAATTTTAAAGGGTCCCTTGGCAATGATCAATATTTGGAATATTAAT 312
Db 229 GATCGAATATCTAGAGACTTTTAAAGGGTCCATTTGCTATGATGATGATGATGATGAT 288
Qy 313 AGGCTAATGGTATTTTATGGGAG-----GGCTGATCATTTGAGACCTTAATGGTT 366
Db 289 TTCATTTGTTGTAATTAATGAGCGGTCAAGAGCGTATGATATGAGGAGAAATTAAGAA 348
Qy 367 CTGTTGAAGAGCTTATTAAGAAAGTATGATCAGCGTATAGAGAAATGCTCTTGA 426
Db 349 CGATGGAAGAACTCGTTGATCAAAAATAGAAATATATGATTAAGTAAAGCTCTTGGT 408
Qy 427 GACTAGAAAGTTTACAGGGAATTAATGATGATATATCAATATGACTGCAGATGGCTA 466
Db 409 GAATTAAGAGGCTAGAAATGCTTTGATGATATCAGCAGATCAGTTGAAGATTTGGCTG 468
Qy 487 GTTAACAAGATGATG---ACATCGAGGGCCTAGTAAACGAGTATGCAATTTGAT 543
Db 469 GAAATCGCAATGATCAAGAACTAGAAAGTGTGTTCTAATCAATTTATAGCTTAAGT 528
Qy 544 AACTTTTCAAAAAGATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTTA 603
Db 529 CTTAATCTTTGTTAGTTCAATTCATCTTTTGGAGTATCCGAGACAGAAATGATTAATTA 568
Qy 604 CAGATATATGACAGACCGGGAATTTGATTAATTTTATTAAGAGATGCTATTAATTT 663
Db 589 GCAGTATATGACAGAGCTGGAACCTACATTTATTTTATTAAGAGATGCTTATATTTT 648
Qy 664 GAGGACAGTGGCAATTTAGTGAATGATGAAATTCGATATTAATTAATGACATCAAGGA 723
Db 649 GAGGAAGAGTGGGATTTACACAGAGTGAATTTCTAATTTATATATGCTCAAGTGCA 708
Qy 724 CTGATTAAGAAATATTAAGATCTTATTAATCAATCTATTAACAGAGGTTTAAATCAATTT 783
Db 709 CTTACCGCTGAATATCAAGCTATTTGTGTAAGTGTATTAATTCGCTTAAATTTG 768
Qy 784 AATGCTCAATGCTCAAGATTTGGTGAAGCTTTAATAGTTTGTACAGATATGACATTA 843
Db 769 AAGGTACACCTTCAAAAGTTGGCTGAATTAATCATCAGTTCCGTAGAGATGACATTA 828

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QY 844 ACAGTATGATCTCGCAATATTATTTCCAACTATGATCCAGTAGGTAATCCATTAGCA 903
 DB 829 CTGGTATTGATTTGGGCGGTATTTCCTAACTATGACACATATGATATCCATCGAA 888
 QY 904 GTTAAACCGAATTGCTAGGGAAGTTATACAGATCCAGTAGGTTTACTGGGGATTA 963
 DB 889 ACAACAGCTCACTTACAGGGGATGTATACAGATCCGATTAACATATGAGACA 948
 QY 964 GAAAGTAGAGTAGGACTTACCTTGATATCTATATATCAACTTAACTTACCTGCTATG 1023
 DB 949 AGTACTGAGATTCTGCA---ACCTTGGTCAACCCACAGTGTATCTCTTTTATGAAGTT 1005
 QY 1024 GAAATTAACGCAAGACAGCTCTTCTTATACACTTGGTTATGCTATTTTGTATAT 1083
 DB 1006 GAAACAGCTATTTGTCGCGCACACTTGTGTATATCTAGCTCAGTAGAATTAAT 1065
 QY 1084 ACAAGACTCTAGTAAATATGT-----CTGATGTAGAAATTTTGGGAGGGCAT 1134
 DB 1066 ACAAGTAGAGGGGTATTTAGTAAATATGATGCAATATTAACCTACTGCTCAGACAT 1125
 QY 1135 ACATAGTTGAAATGGAATGATGGTCTGAAATTAACCACTTAAGTTGGTAAACCTGAT 1194
 DB 1126 ACCCTAAATATCTGTGAAACAGCTGATTCGACCTTAACATACACACTAATTACGCTCA 1185
 QY 1195 TCTATTACTCTTATTCATATTTTAAATTTTCGCAACCTTCTGTTTCACTATTTAGTCA 1254
 DB 1186 ATCACTTCAGAAAGAAATTCATTGCTGAGATGAGGATATTTTGAATTAATTTCA 1245
 QY 1255 CTTCCTCTGATATTTTGAAGAGAACAGAGCTTAATATTTATTTACTAGTCACTATGCA 1314
 DB 1246 ACTGTGCA---ACCTAGCTAATTTACTACAAAGGCAATATGTTGCGGGATCTTGG 1302
 QY 1315 GTCTCGAGATTTATTTTAAATATCATCAATATTAATATGATCTGATCTTAAAGATAC 1374
 DB 1303 TTTCATATGTAAAAAGGGAACCTCATCAACAGCGATTTATTTAAAAACACAT 1362
 QY 1375 GAAGTCTGCTAATCTTCCATCCAAACTAATATATCAGAAATTTACAGAAAGATAG 1434
 DB 1363 ACAGCTCTCAAGAGGTGACAGAGTTTATGATCAAGTATGAATACTCTAGATAG 1422
 QY 1435 CCAAGCAACCAAGCAGAGATTTCCAGCCATATGATTTCTTATATATCAATTTGATGCA 1494
 DB 1423 ACTGTACCGGTACTGAAGCTATGATCATGATATTTCTCATATTTACCTCCATCTTTC 1482
 QY 1495 CGGCAAGTAGTTCAGGCGGTATTTAGTCTTTTAAAGTTTGGGGCACAATCCAGT 1554
 DB 1483 TCTAAATATGGAGTGCATATGAGAGTTTCCCTGTATTTTGTGGACACATCTAGT 1542
 QY 1555 ATGATCTGATATATCGTCTTGAACAGATTAATTAATCAAAATAGATGCAATTAAGT 1614
 DB 1543 GCGGATTTAAATATCAATATATATGATTAATATCACTCAAAATCCAGCGGTAAAGGA 1602
 QY 1615 TGGGGGGGAATTCGGGTTTGTATCCAGACACTACTGG 1655
 DB 1603 GACATGTATATCTAGGGGGTTCGTATGATCAGGGTCTTGG 1643

RESULT 6

AAQ28940 standard; DNA; 3471 BP.

AAQ28940;

24-FEB-1993 (first entry)

B.churingiensis PS50C insecticidal protein gene.

B.t.PS50C; NRRL B-18746; pMYC1638; Colorado potato beetle;

Coleoptera-active toxin; ss.

Bacillus thuringiensis.

XX

FH Key Location/Qualifiers
 FT mat_peptide 1..3471
 PT /*tag=a
 FT /product="toxin"
 FT /note="active against Coleoptera"

CA2059242-A.

17-JUL-1992.

13-JAN-1992; 92CA-02059242.

16-JAN-1991; 91US-00642112.

02-JAN-1992; 92US-00812180.

(MYCO) MYCOGEN CORP.

Foncerrada L, Sick AJ, Payne JM;

WPI; 1992-323784/40.

P-PSDB; AAR27343.

New Bacillus thuringiensis isolate - used for preparing toxin, DNA and transformed hosts for controlling coleoptera insect pests.

Claim 13; Page 18-20; 33pp; English.

Total cellular DNA was prepd. from B.t. PS50C. The DNA was partially

digested with Sau3A and 9-23kb fragments were ligated into BamHI-

digested lambda GBM-11. Packaged phage were plated on E.coli KM251 cells

and screened using a radiolabelled probe. Positive plaques were purified

and rescreened. Single isolated purified plaques were used to infect

E.coli KM251 in liquid culture. DNA was isolated, digested with XhoI and

large fragments ligated to XhoI-cut pHTBlueII. The ligation mixt. was

introduced into competent E.coli NM522 cells. Plasmid pMYC1638 contained

a 12kb XhoI insert from which the 3471bp sequence of the toxin gene was

determined

Sequence 3471 BP; 1202 A; 570 C; 745 G; 954 T; 0 U; 0 Other;

Query Match 12.5%; Score 256.2; DB 2; Length 3471;

Best Local Similarity 50.5%; Pred. No. 2,9e+49;

Matches 888; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

QY 13 AAAAAATTAATGAATATGAAATGTTGATGCTTAAAGATCAACTTAATATGCTAAT 72
 DB 10 AATTAATCAAAATGAATATGAATTAATATGATGCGACCTTATCATC--TGTATCCAGT 66
 QY 73 TGTATCCAAAGTATCTAGTCAACAAAGATCCCAAAATGACTATGCGAAACGAACTAT 132
 DB 67 GATTTCAACAGATACCTTTTGCAGATGAGCCAAACGATGCGTTACAAAATATGAATTAAT 126
 QY 133 AAGAAATGCTAAATATGTGTGATTCAAATATCAATTTATTTGATATTAAGCAGTAT 192
 DB 127 AATGATTTATCTGAATATGTCTGG-----GGAGAAATCTGTAATTA 168
 QY 193 TCTAGCCCTGAAGCTGCTTAAAGTATGATGATGCTGTTTAAACGGTATTAACAGTGA 252
 DB 169 TTTGAAATCCGAGAGCGTTTATATGATTCATCAAGATTCAAACTGGAATTTGCAATGTT 228
 QY 253 GGGACTATATCTTCAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAATTAATAGT 312
 DB 229 GGTGCAATATCTAGAGCTTTAGGGGTTCCATTTGCTAGTCAAGTATACCTGTTTCTATAGT 288
 QY 313 AGGCTAATAGTATTTTATGGGCAG-----GGCTGATCATTTTAAGCACTTATAGTT 366
 DB 289 TTCATTTGTTGTCATTTATGCGCGTCAAAAGAGCTGATATATGAGGAGAAATTAATGAA 348
 QY 367 CTGTTGGAAGAGCTTATTAAGAAAGTATATGATGATGATGATGATGATGATGATGATGAT 426
 DB 349 CGATGGAAGAACTGTTGATCAAAAAATATGTAATAATATGATTAAGGCTCTTGGCT 408
 QY 427 GACCTAAGAGCTTTACAGGGAATTAATGAGATATATCAAACTAGACTGCAAGATGGCTA 486

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Db      409  GAAATTAAGGGCTAGAGAAATGCTTGGATGTATATACAGAGTCACTTGAAGATGGCTG 468
Qy      487  GTTAACAGAAATGATG---ACAAACGAGGCGCATATACGAGATATGCAATTTGAT 543
Db      469  GAAATTCGCAATGTATGAGAAATGAGATGTGTCTTCTATCAATTTATATGCTTAAT 528
Qy      544  AACTTTTTCGAAAAGAAATATGCGCAAAATTCAGAGAAAGAAACCTTGAATTTTATG 603
Db      529  CTTAATCTTTGTATGTTCAATTCATCTTTTGCAGATATCCGAGACGAGATCTATTTA 588
Qy      604  CCAATATATGACAAAGCCGCAATTTGCAATTTAATTTTATTAAGATATGCTATTTT 663
Db      589  GCAATATATGACAGCGCTGTAAACCTTACATTTATTTGATTAAGATATGCTTCAATTT 648
Qy      664  GAGACAGATGCGCAATTAAGATGATGAAATTCGTATATATTTATCAAGATCAAGGA 723
Db      649  GAGAGATGAGGGGATTTTACACAGGTGAATTTCTAGATTTTAAATCGTCAAGTCAA 708
Qy      724  CTGATTAAGAAATATTAAGATCATTTGTATATCATTTATTAACAGGCTTAAATCAATTT 783
Db      709  CTTAACCGCTGATATTTTCAAGATATTTGTATTAAGGTATTAATAATCGCTTATTAAT 768
Qy      784  AATCGCTCAATATGCTCAAGATGGGTGAGCTTAAATAGTTTCGTACAGATATGACATTA 843
Db      769  AAGGTACCACTTAAAGATGGCTGATATATCATCATGATTCGTAAGAGATGACATTA 828
Qy      844  ACAGATATTAAGTCTCGCAATTTATTTCCAACTATATGATCAAGATATGCTTATGCA 903
Db      829  CTGATATTAAGTTGATGGCTTATTTTCCAACTATATGATCAACATATGATTCATGAA 888
Qy      904  GTAATAACGGAATGACTAGGGAAGTTTATATACAGATCAAGATGAGGTTTATCGGGTATTA 963
Db      889  ACAATACCTCACTTACAGGAGATGTATATACAGATCGATATTAACATATGATGACA 948
Qy      964  GAAAGTGAAGTGAAGTACTTACCTTGTATATATCTAATATACACCTTACTGATAG 1023
Db      949  AGTACTGGATTTGCA---ACCTTGGTCAACCAAGTGGTATCTTTTATTAAGATTT 1005
Qy      1024  GAAATTAACGCAAGACAGCTCTTCTTATATACACTTGGCTTATCGTATTTTGTATAT 1083
Db      1006  GAAATTAACGCAATATCTCTGCGCACACTTGTATATCTACAGCTCAGATGAATTAAT 1065
Qy      1084  ACAAGGCTCAGGTATATATGCT-----CTGATGGAATATTTTGGGCGAGGCAAT 1134
Db      1066  ACAAGTGAAGGGGTATTAAGTAAATATATGATCATATTAATCTAGCTGACAGAT 1125
Qy      1135  ACAATTAAGTGAATATGATGTTCTGAAATTAACCCATTAATCTTGTGTAATATGAT 1194
Db      1126  ACCCTTAATATATCTATAGAACAGCTGATTTGACCGTATATACAGCTAATTAACGTCGA 1185
Qy      1195  TCTATTAATCTCTATTAATATTTTAAATTTGCGGAACCTTCTGTTTCAAGTATGATCA 1254
Db      1186  ATCACTTCAAAAAGAAATTCATTTGCACTTGAAGATGGGATATTTTGAATTAATTTCA 1245
Qy      1255  CTGCTGCTATATATTTTAAGAGAAACAGAGCTAATATATATTAATTAAGTCAATGATGA 1314
Db      1246  ACTGTGCA---ACCTAGCTAATTAATCAAAAAGCATATGATGTCGGGATCTTGG 1302
Qy      1315  GTTCGAGAGTTATTTTATATACATCAAAATTAATATATGATCACTTTTAAAGTATAC 1374
Db      1303  TTTCATATATGTAATAAAGGCAACCTCATCAACAAACAGCTATTTATATTAATAAACAAT 1362
Qy      1375  GAAATGCTGTATATCTTCCATCCCAACTATATTAATTAATTAATTAATTAATTAATTA 1434
Db      1363  ACAGCTCTCCAAAGGTATACACAGTTATATCAAGATGAAATTAATCTCTAGATGA 1422
Qy      1435  CCAAGACCAAGAGAGATTTAGCCATATATCTTATATATCAAAATTTTATGATGA 1494
Db      1423  ACTGTACCGGTAGTGAACCTATATGATATATCTCATATTAATCTCCCATTTCTTC 1482
Qy      1495  CGGCAAGTATGATGAGCGGTATTTAGTCTTTTAAAGTTTGGGCAATACAGAT 1554

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Db      1483  TCTAAAAATGGAGTGCATATATGAGAGTTTCCCTGATATTTGTTTGACACATACTAGT 1542
Qy      1555  ATGATCGTATATATGCTTCTTGAACGATATAAATTTACTCAATATAGATGCAATTAAGT 1614
Db      1543  GCGATTTAATATATATATATATATATATATATATATATATATATATATATATATATAT 1602
Qy      1615  TGGGGGGGGAATATCGGTTTGTATCCAGACCTACTGG 1655
Db      1603  GACATGTTATATCTAGGGGGGTTCGTATGACAGGTCCTGG 1643

RESULT 7
AA038653
ID AA038653 standard; DNA; 3471 BP.
XX
AC AA038653;
XX
DT 25-MAR-2003 (revised)
DT 15-JUL-1993 (first entry)
XX
DE Bt isolate Pes0C coding sequence.
XX
KM Lepidopteran-active; toxin; Ti; Ri; plant; cell; Bt; ss.
XX
OS Bacillus thuringiensis.
XX
PN MO9304587-A1.
XX
PD 18-MAR-1993.
XX
PF 11-SEP-1992; 92MO-US007697.
XX
PR 12-SEP-1991; 91US-00758020.
PR 08-SEP-1992; 92US-00941650.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Uyeda KA, Bradfish GA;
XX
DR WPI; 1993-100566/12.
XX
DR P-PSDB; AAR33768.
XX
PT Controlling lepidopteran pests - using compsn. of Bacillus thuringiensis
PT strains or plants or microorganisms transformed with their toxin genes.
XX
PS Claim 12; Page 20-22; 38pp; English.
XX
CC The sequences given in AA038653-55 encode lepidopteran-active toxins.
CC These sequences were used within a Ti or Ri plasmid to transform plant
CC cells. Whole plants can then be regenerated from the transformed cells.
CC The toxin may also be produced by cloning Bacillus thuringiensis (Bt).
CC It may then be applied directly to the plant locus. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 3471 BP; 1200 A; 567 C; 751 G; 953 T; 0 U; 0 Other;

Query Match 12.5%; Score 256.2; DB 2; Length 3471;
Best Local Similarity 50.5%; Pred. No. 2.9e-49;
Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

Qy      13  AAAAAATAAATGAATATGATGATGCTTTAAGATCAACTTAATATGCTTAAT 72
Db      10  AATATATCAAAATATATGAAATTTATATATGATGACACCTTCTATCATC---TGTATCAGT 66
Qy      73  TGTATCAAGATATCTTACAGCAAAAGATCCAAATGATATATGCAAAACAGAACTAT 132
Db      67  GATTTTAAAGATATACCTTTTGGCAATGAGCCAAACAGATCGTTTAAAAAATATGAATAT 126
Qy      133  AAGGAATGGCTAATATATGATGATTCAAATATACAAATTTATGATATTAAGACGAT 192
Db      127  AAGATATATGAAATATGCTGGG-----GAGAGAAATCTGGAATTA 168
Qy      193  TTTAGCCCTGAAGCTGCTTAAGTATGATGATGATGCTGTTTAAAGGATATTAACAGTGA 252

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Db      169  TTTGGAATTCGGAGACGTTTATTAGTTCACGATTCGAACTGGAATTTGGCATTTGTT 228
Qy      253  GGGACTATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCATTCATTTGGAAATATATAGT 312
Db      229  GGTGCAATCTAGAGAGCTTTAGGGGTTCCATTGTCTAGTCAGATAGCTATGTTCTATAGT 288
Qy      313  AGGCTAATAGTATTTTATGAGGAG-----GGCCTGATCCATTTGGAAGCACTTATGTT 366
Db      289  TTCAATGTTGTCATATATGCGCGTCMAAGCGTATGATATATGGGAGAAATTTATGAA 348
Qy      367  CTTGTTGAAGAGCTTATTAAGAAAGTATGATCAGGCTGTAAGAGAAATGCTCTAGA 426
Db      349  CGAGTGAAGACTCGTTGATCAAAAAATATGTAATTAAGATTAAGGCTCTTGCT 408
Qy      427  GAGCTAAGAGTTTACAGGGAATTTATGAGACTATATCAAACTAGACCTGACAGCTGCTA 486
Db      409  GAATTTAAAGGCTTAGAAATGCTTTGAGATGATATACAGACATCTGTAAGAAATGGCTG 468
Qy      487  GTTAACAAAGATGATG---ACAAATCGAGGGCACATGATAACGAGATGCAATGTTGAT 543
Db      469  GAAATTCGCAATGATGCAAGAACTAGAAAGTGTGTTCTAATCAATTTATAGCTTAGAT 528
Qy      544  AACTTTTGAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
Db      529  CTTAATCTTGTATTCATTTCAATTTCAATTTTGCAATCCGAGATCCGAGACAGAACTATTA 588
Qy      604  CCAGTATATSCAAGACCGCGAAATTTGCAATTTTATTTATTAAGAGATGCTGATTTAT 663
Db      589  GCGATATATGCAACGCTGTGAACCTACATTTATGTTATTAAGATGCTTCTATTTT 648
Qy      664  GGAGCAGATGGCAATTTAGTGATGATGAATAATTCGTGATTAATATACAGACTACAGGA 723
Db      649  GGAGAAAGATGGGAGATTTACACAGGTGAATTTCTAGATTTATATGCTCAAGTGCA 708
Qy      724  CTGATTAAGAAATATTAAGATTCATGTTAATCAATTCATTAACAGGTTTAAATCAATTT 783
Db      709  CTTACCGCTGAATATTCAGCTATGTGTAAGAGGTATTAATAATCGGCTTAGATTAATG 768
Qy      784  AATCGCTCAATGCTCAAGATTTGGGTAGGCTTTAATGATGTTTGTACAGATATGACATTA 843
Db      769  AAGGTATCCACTTTAAAGTTGGCTGATATTCATCATAGTTCCGTAGAGAGATGACATTA 828
Qy      844  ACAGTATTAATGATCTCGCAATATTTATTTCCAACTATGATCCAGTATGATTCATTAGCA 903
Db      829  CTGATTAATTAATTTGGTGGCTTATTTCCAACTATGATCACATATGATTCATCAATCGAA 888
Qy      904  GTTAAAAACGAAATTTGACTAGGGAAGTTTATACAGATTCAGTATAGGTTTACTGGGATATA 963
Db      889  ACAACAGCTCACTTACACGCGGATGTGTATACAGATCCGATACATTTTAAATATGACGA 948
Qy      964  GAAAGTGAAGGTAGACTTACCTTGGTATATCTTAATATATCAACTTTACTGCTATG 1023
Db      949  AGTACTGATCTTGCA---ACCTTGTGTCACCCACAGTGTATCTTTTATGAAGTT 1005
Qy      1024  GAAATATACGCAAGACGCTCTTCTTATACCACTTGCTTATATGCTATATTTTGTATAT 1083
Db      1006  GAAATCAACGTAATTCGTCGCGCACACTTGTGATATACTACGCTCAGTAGAAATTAAT 1065
Qy      1084  ACAAGACTCTAGTATATATG-----CTGATGTGAAGAAATTTTGGGAGGGCAT 1134
Db      1066  ACAAGTAGAGGGGTATTTACGTTAAATATATGATGCAATATTAACCTACGTCAGGACAT 1125
Qy      1135  ACATTAATGTAATGGAATGATGTTTGAATAATACCATTAATCTTTGGTAAACCTGAT 1194
Db      1126  ACCCTTAATAATATGTAGAACAGCTGATTCACCGTAAATACACAGTAAATTCGCTCGA 1185
Qy      1195  TCTATTACTCTTATTCATATTTTAAATTTTGGCAACCTTTCTGTTTTCAGATATGATCA 1254
Db      1186  ATCACTTGAAGAAAGAAATTCATTTGCACTTGAAGATGAGGATATTTTGAATTAATTC 1245
Qy      1255  CTTGCTCTATATATTTTGAAGAGAACAGGCTAATATTAATTTACTAGTACGTATGGA 1314

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Db      1246  ACTGTGGCAA---ACCTAGCTAATTACTACCAAAAGCATATGTGTGCGGATCTTTGG 1302
Qy      1315  GTCTCGAGAGTTATTTTATATACATCAAAATATATAATATGATACCTGATCTTTAAGATAC 1374
Db      1303  TTCATATGTTAATAAAGGGAACTTCATCAACAAACGCGATTTATATTCAAAAACACAT 1362
Qy      1375  GAAGTGCCTGCTAATTTTGCATCCCAACTATATTTATCGAAATTTACAGAAAGATAG 1434
Db      1363  ACAGCTCTCCAAAGGGTATACAGAGTTTATGATATCAAGTATGAATAATACCTTAGATAGA 1422
Qy      1435  CCAAGACCAAAACGACAGAGATTTACAGCATAGATTAATCTTAATATCAAAATTTGATGCA 1494
Db      1423  ACTGTACCGGTACTGAAAGCTATATGCTATGATTTCTCATATTTCATCCCATTTCTTC 1482
Qy      1495  CCGCGAAGTATGTTACAGCGGTATTTGTATGTTTAACTTTTAACTTTGGTGGCACATACAGT 1554
Db      1483  TCTAAAAATGGGAGTGCATATATAGGAGTTTCCGTATTTGTTTGGACACATACATAGT 1542
Qy      1555  ATGATCTGATATATGTTGCTTTGAAACCAATTAATAATTTACTCAATATAGATGATTAAGCT 1614
Db      1543  GCGGATTTAAATATATCAATATATTCAGATTAATAATCACTCAAAATTCACGCGTAAAGGA 1602
Qy      1615  TGGGGGGGAATATCGGTTTGTGTCATCCAGACCTACTGG 1655
Db      1603  GACATGTTATATCTAGGGGTTCCGTATGTAACAGGTTCTGG 1643

RESULT 8
AAT43222
ID  AAT43222 standard; DNA; 3471 BP.
XX
AC  AAT43222;
XX
DT  16-OCT-2003 (revised)
DT  28-JAN-1997 (first entry)
XX
DE  Anticrabab pest toxin 50C(a) coding sequence.
XX
KW  Toxin 50C(a); scarab pest; toxin; insect; scarabaeidae; pest control;
KW  larval stage insect; grain; tuberous crop; white grub; chafer grub;
KW  cyclocephala; popillia; ds.
XX
OS  Bacillus thuringiensis; strain kumamocensis.
XX
PN  US554534-A.
XX
PD  10-SEP-1996.
XX
PF  30-SEP-1994; 94US-00315468.
XX
PR  16-DEC-1991; 91US-00808316.
PR  30-JAN-1992; 92US-00828430.
PR  01-FEB-1993; 93US-00014941.
XX
PA  (MYCO ) MYCOGEN CORP.
XX
PI  Foncerrada L, Narva KE, Michaela TE;
XX
DR  WPI: 1996-424659/42.
XX
P  P-PSDB; AM06418.
XX
PT  New nucleic acid encoding B. thuringiensis toxin active against scarab(s)
PT  - also related toxin and transformed microbes, effective against adult
PT  pests and their larvae.
XX
PS  Example 2; Col 17-20; 24pp; English.
XX
XX  AAT43221-743223 represent the coding sequences for toxins that are active
XX  against scarab pests. This sequence was isolated from the Bacillus
XX  thuringiensis strain kumamocensis. Insects in the family Scarabaeidae
XX  constitute a serious pest control problem, especially when destructive
XX  larval stage insects infest high value turf found in golf courses,
XX  playing fields and lawns. The larvae of many species also attack grains,

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CC tuberous crops, and ornamentals. The larvae are known as white grubs, or
CC chafers grubs, and can be found in decaying organic matter, or in the soil
CC where they consume plant roots. In Europe and the U.S. populations of
CC these larvae and adults have developed resistance to chemical
CC insecticides such as the organochlorines and DDT. The toxins encoded by
CC these sequences, and intact cells that are capable of expressing the
CC proteins, can be used to control many pests of the family scarabaeidae,
CC such as species of Cyclocephala, and Popillia. The toxins are active
CC against larvae (present in soil) and against adults. (Updated on 16-OCT-
CC 2003 to standardise OS field)

XX Sequence 3471 BP; 1200 A; 567 C; 751 G; 953 T; 0 U; 0 Other;

Query Match 12.5%; Score 256.2; DB 2; Length 3471;
Best Local Similarity 50.5%; Pred. No. 2.9e-49;
Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

QY 13 AAAAAATGAATATGAATGTTGATGCTTTACGAATCACTTAATATGCTTAAT 72
DB 10 AATTAATCAAAATGAAATGAAATTAATGATGCGACACTTCTACATC---TGATCCAGT 66
QY 73 TGTATCCAGGATCCACTAGCAAAAGATCCCAATGACTATGCAAAACAGAACTAT 132
DB 67 GATTTCAACGATACCTTTTGGCAATGACCAACAGATGCTTACAAATATGAAATAT 126
QY 133 AAGAATGCTAATATGATGATGATCAATATCAATTTATGATATTAAGACAGTAT 192
DB 127 AAGATTTATGAAAATGTCTGG-----GAGAGAAATCCGAAATTA 168
QY 193 TCTAGCCCTGAAAGCTGTTTAAGTGAAGATGCTGTTTAAACGGATTTAAACAGTGA 252
DB 169 TTGGAATCCGAGAGAGTTTATTAAGTTCACGATCAAACTGGAAATTTGCAATGTT 228
QY 253 GGAATATATCTTTCGAATTTAGGGGTCCCTTGGCAAGTCAATCATTTGAAATTAAT 312
DB 229 GGTGCAATACAGAGCTTTAGGGGTTCATTTGCTAGTCAATAGTAACTTTCTAATAGT 288
QY 313 AGGCTAATAGATATTTTATGGGAG-----GGCTGATCCATTTTGAAGCACTTAATGTT 366
DB 289 TTCAATGTTGTCAATTTATGCGCTCAAAAGCGTATATATAGGGAGAAATTAAGAA 348
QY 367 CTGTTGAAGAGCTTATTAAGAAAGATATAGATCAGCGTGAAGAAATGCTCTTGA 426
DB 349 CGAGTGAAGAACTCGTTGATCAAAAAATGAAAAATATATTAAGTAAGGCTCTTGGT 408
QY 427 GAGCTGAAGGTTTACGGGAATTTATGAGCTATATCAAACTGACGCAAGATGCTGA 466
DB 409 GAATTAAGAGGCTAGGAAATGCTTGGATGATATCAGCAGTCACTTGAAGATGGCTG 468
QY 487 GTTAACAGAAATGATG---ACAATCGAGGGGCACTAGTAAACGAGTATGCAATGTTGAT 543
DB 469 GAAATTCGCAATATGCAAGAACTAGAAAGTGTGTTTCTAATTAATTAAGCTTAAT 528
QY 544 AACTTTTTCGAAAGATATGCAAAATTCAGAGAAAGAACTTTGAATTTATGTTA 603
DB 529 CTTAACTTTGTTGTTCAATTCATCTTTTGCAAGTATCCGAGACAGAAATGATTAATTA 588
QY 604 CCAGTATATGCAAGACCGGAAATTTGCAATTTATTTATTAAGAGATGCTGATTAATTT 663
DB 589 GCAGTATATGCAAGCGTGTGAACCTAATTTATGTTATTAAGAGATGCTCTAATTTT 648
QY 664 GAGAGCAGTGGCAATTAAGTGAATTCGATTAATTAATTAATCACTTACAGGA 723
DB 649 GAGAAAGAGTGGGATTTTACACAGGTGAATTTTCTAGATTTATTAATTCGTCAGTGCAA 708
QY 724 CTGATTAGAGAAATATTAAGATCATTTGATTAACATTTCTATTAACAGAGGTTTAAATCAATTT 783
DB 709 CTTACCGCTGAATATTCAGACTATTTGTTAAAGTGATTAATTAATTCGGCTTAAGTAAATTTG 768
QY 784 AATCGCTCAAAATGCTCAAGATTTGGGTGAGCTTTAATATGTTTGTATGAGATATGACATTA 843
DB 769 AAGGTAACCACTTAAAGTTGGCTGAATTAATCATCATGTTCCGTAGAGAGATGACATTA 828

QY 844 ACAGTATTAGATCTCGCAATATTAATTTCCAACTATGATCCAGTAGATTAATCCATTAACA 903
DB 829 CTGATTTAGATTTGGGCGGATATTTCCAACTATGACACATATATGATTCAAATCGAA 888
QY 904 GTAAAAACGAATTTGACTAGGGAATTTATACGATTCAGTATGAGTTTACTGGGATTTA 963
DB 889 ACAACAGCTCAACTTACACGGGATGATATACAGATCCGATTTTAAATCAATAGTACA 948
QY 964 GAAAGTGAAGGTGAGACTTACCTGATATATCTTAATATCAACTTACTGCTATG 1023
DB 949 AGTATGATTTTCGCA---ACCTTGGTCAACCAAGTGTATTTCTTTTATGAAGTT 1005
QY 1024 GAAATATACGCAAGACGACGCTCTTCTATATACACTTGGCTTAATGATATTTTATAT 1083
DB 1006 GAAATCAAGTAAATTTGTCGCGCACACTTGTGATATATCTACCTCAGTAAATTAAT 1065
QY 1084 ACAGAGCTCTAGTAAATATG-----CTGATGTGAATATTTGGGAGGCGAT 1134
DB 1066 ACAAGTGAAGGGGATTTACGTTAAATATGATGATATATTAATCACTAGTCAAGACAT 1125
QY 1135 ACATTAAGTTGAAATGAAATGATGATGTTCTGAATATACCAATTAACCTTTGGTAAACTGAT 1194
DB 1126 ACCCTAAATATATGTAAGACAGCTGATTCGACCTTAACATACAGCTAATTAACGTTGCA 1185
QY 1195 TCTATTACTCTTATTCATATTTTAAATTTTCGCAACCTTCTGTTTCAGATATGATCA 1254
DB 1186 ATCACTTCAAGAAAGAAATTCATTTGCACTTGAAGATAGGGAATTTTGAATTAATTA 1245
QY 1255 CTGCTGCTATATATTTTGAAGAGAACAGAGCTTAATATATTTACTAGTCAATGTA 1314
DB 1246 ACTGTGGCAA---ACCTAGCTAATTAATCTACCAAAAGCAATATGTTGCGGATCTTGG 1302
QY 1315 GTCTGAGAGTTATTTTAAATATATCAATATTAATATGATCTGATCTTAAGTATAC 1374
DB 1303 TTCAATATGTAATTAAGGGAACTCATCAACAACGCTATTTATATTAATTAATTAACAT 1362
QY 1375 GAAGTCTGCTATATCTTCCATCCCAACTATATTTATGAAATTTACAGAAAGATTAAG 1434
DB 1363 ACAGCTCTCAAGAGGTATACAGAGTTTATGATTAAGATGAATTAATCTAGATTAAGA 1422
QY 1435 CCAAGACCAACGACAGAGATTTTACGCAATATTTATTAATTAATTAATTTTGAATGA 1494
DB 1423 ACTGTACCGGTACTTAAGCTATAGTATGATTAATTCATATTTCTCCATTTCTTC 1482
QY 1495 CGGGAAGTATTCAGGCGGATTTGTTAGCTTTTAAAGTTGGTGGGACATACAGAT 1554
DB 1483 TCTAAATTAAGGAGTGCATATATGGAAGTTTCCCTGATTTTGTGGACACATACAT 1542
QY 1555 ATGATCGTATATATGCTCTTGAACAGATTAATTAATTAATTAATGATGAGTTAAAGGT 1614
DB 1543 GCGGATTTAAATTAATTAATTAATTTCAAGATTAATTAATTAATTAATTAATTAATTA 1602
QY 1615 TGGGGGGGGAATATCGGTTTGTATCCAGACTACTGG 1655
DB 1603 GACATGTTATATCTAGGGGGTTCGTAATGATCAAGGCTCTGG 1643

RESULT 9

AA051704
ID AA051704 standard; DNA; 3471 BP.

XX AA051704;

AC 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DE 09-DEC-1995 (first entry)

XX Bacillus thuringiensis crystal protein P550C gene.

XX Crystal protein; delta endotoxin; acaricide; pesticide;

XX biological control agent; transgenic plant; crop improvement; ds.

OS Bacillus thuringiensis serovar kumamotoensis; (isolate P550C).

Db 1543 GCGGATTTAAATATACATATATTCAGATTAATCACTCAAAATTCAGCGGTAAAGGA 1602

Qy 1615 TGGGGGGGGAATATCGGGTTTGTTCATCCAGACCTACTGG 1655

Db 1603 GACATGTTATATCTAGGGGGTTCGGTAGTACAGGGTCTTGG 1643

RESULT 10

ABK51132

ID ABK51132 standard; cDNA; 3690 BP.

AC ABK51132;

XX 30-JUL-2002 (first entry)

XX cDNA encoding *Bacillus thuringiensis* insecticidal protein.

XX Insecticide; transgenic; Coleoptera larvae; ss; gene.

XX *Bacillus thuringiensis*.

XX Key Location/Qualifiers

FT CDS /tag= a /product= "Insecticide protein"

XX JP2002045186-A.

XX 12-FEB-2002.

XX 03-AUG-2000; 2000JP-00236140.

XX 03-AUG-2000; 2000JP-00236140.

XX (SDBS-) SDS BIOTECH CORP.

XX MPI; 2002-356468/39.

XX P-PsDB; AAU80281.

XX A protein having insecticidal activity, a DNA encoding said protein, and an agent and a method for preventing harmful organisms.

XX Claim 4; Page 17-18; 19pp; Japanese.

XX This invention relates to a crystalline protein comprising a fully defined sequence and the nucleotide sequence encoding this protein. The protein of the invention is an agent for preventing harmful organisms comprising *Bacillus thuringiensis* serovar *Galleriae* SDS502, its mutant or a microbe transformed by a DNA encoding the protein. This microbe can be used to produce a protein containing the protein, or containing a protein having insecticidal activity produced by the SDS502, its mutant or a transformed microbe, a microbe which is transformed by using the above DNA and produces the above protein having insecticidal activity, a plant or a seed transformed by using the above DNA, and *Bacillus thuringiensis* serovar *Galleriae* SDS502 producing a protein comprising and producing a protein showing insecticidal activity. The protein of the invention may have insecticidal activity. The agent is used for preventing Coleoptera larvae. This sequence represents the cDNA encoding the *Bacillus thuringiensis* insecticide protein of the invention

XX Sequence 3690 BP; 1289 A; 599 C; 762 G; 1040 T; 0 U; 0 Other;

Query Match 11.5%; Score 236; DB 6; Length 3690; Best Local Similarity 55.9%; Pred. No. 1.5e-44; Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

Qy 13 AAAAATAAATGAATGAATGATGCTTTAGCAATCACTTAATATGCTTAAT 72

Db 196 AATATATCAATGAATGAATGATGCTTTAGCAATCACTTAATATGCTTAAT 252

Qy 73 TGTATTCAGAGTATTCAGCAAAAGATCCAAATGCTATGCGAAACAGAACTAT 132

Db 253 AATTCGTATGATACCTTATGCAAAAGATCCAAATGCTATGCGAAACAGAACTAT 312

Qy 133 AAAAATGCTTAATATGCTGATTCAAATATACAAATTAATGCTATATACAGCTAT 192

Db 313 AAAATATATCTGAATATGCTGAG-----GGAAGAAATCTGAATTA 354

Qy 193 TCTAGCCCTGAAGCTGCTTTAAGTACAGAGATGCTGTTTAAACGGTATTAACAGTGA 252

Db 355 TTTGAAATCCGAGAGCTTATTAATGATCAATCAAGCTGAATCTGAATATGCAATGTT 414

Qy 253 GGAATTAATCTTGAATTTAGGGGTCCCTTGGCAAGTCAATCTTGGAAATTAATAGT 312

Db 415 GGTCAAGTACTGGGGGCTTTAGGGGTCCCTTGGCAAGTCAATCTTGGAAATTAATAGT 474

Qy 313 AGCTAATAGTATTTTAATGCGAGGAGCT-----GATCAATTTGAGCACTTAATGTT 366

Db 475 TTGATGTCGGTCAATTAATGCGATCAAGTACCGTATGCTATAGGAAATATGATTCGAAA 534

Qy 367 CTGTTGAAGAGCTTTTAAGAAAGATATGATCAGCGTGTAAAGAAAATGCTCTTGA 426

Db 535 CAAGTGAAGATCTAATTTGATCAAAAATTAACAGATTCGTGAAGAAAACAGCGCTTGA 594

Qy 427 GAGCTAAGAGTTTACAGGGAAATTAATGAGCTATCAACTGAGCTGCAAGCATGGCTA 486

Db 595 GAGCTAAGAGATTTAGAGAGATGCTTAAGCTATATCAAGAAATCACTTAAGAAATGGCTG 654

Qy 487 GTTAACAAGATATGATGACA---ATCGAGGGCACTAGTAACGAGTATGCAATTTGAT 543

Db 655 GAAATCGTATATGATCAAGAGCTAGAGATGTTGTGTGACCGAATATATAGCTTAAG 714

Qy 544 AACTTTTGAAGAAATATTCGCAAAATTCAGAGAAAGAACTTTGAATTTATGTTA 603

Db 715 CTGATTTTGTGCTAAATCCCATCTTTGCAATATCTGACAGAGAAAGTACCATTTA 774

Qy 604 CCAGTATATGCAACAGCGGAATTTGCAATTAATTTTAAGAGTGTGATTAATTT 663

Db 775 TCAATATGCAACAGAGGAAATTTACATTTGCTATATTAAGAGATGCTTCAATTT 834

Qy 664 GGAGCAGTGCATTTAGGTGATGATGAATTCGTGATATATATATATGACATCAAGGA 723

Db 835 GAGAGAGTGGGGATTCACACAGAGAAATTTCCAAATTTATATATGTCAGGTGACA 894

Qy 724 CTGATTAAGATATTAAGATCAATTTGATATCAATTTCTATATCAAGGCTTAATCAATTT 783

Db 895 CGTACCGCCCAATACCTCGATTTATTTGTATTAAGTGTATTAACCTGCTTAGATTAATTA 954

Qy 784 AATCGCTCAAAATGCTCAAGTTGGGTGAGCTTAATATAGTTTGTACAGTATGACATTA 843

Db 955 AAGGTACGAAATGCTCAAGTTGGGTGAGATACCAATTCGAAAGAAATGACATTA 1014

Qy 844 ACAGTATTAATGCTCGCAATTAATTTCCAAATATGATCCAGTATGCTTATGCA 903

Db 1015 CTGATTTAGATTTAGTAGGTTATTTCCAAATATGATCCAGTATGCTTATGCA 1074

Qy 904 GTTAAACGGAATTTGCTAGGAAAGTTTATATGATTCAGTACAGGTTTACTGGGGTATTA 963

Db 1075 ACAACGCGCCCAATTTACAGGAAAGTATATACATCAATATATTAACAGAGAAACA 1134

Qy 964 GAAATGAGGTATGGA 979

Db 1135 AGTGTGATTTTGTGA 1150

RESULT 11

ABK87236

ID ABK87236 standard; DNA; 2003 BP.

XX ABK87236;

XX 07-OCT-2002 (first entry)

XX *Bacillus thuringiensis* Cry1218-1 truncated gene sequence.

XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 XX insect target range; endotoxin; Cry12I8; gene; ds.
 OS *Bacillus thuringiensis*.
 XX MO200234774-A2.
 PN
 XX
 PD 02-MAY-2002.
 PF 24-OCT-2001; 2001WO-US045468.
 PR 24-OCT-2000; 2000US-0242838P.
 XX 23-OCT-2001; 2001US-00032717.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Abbad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 XX WPI; 2002-519178/55.
 DR P-PSDB; AAU99257.
 XX
 PT New isolated pesticidal polypeptide useful for impacting insect pest e.g.
 XX Colorado potato beetle.
 PS
 XX
 PS Claim 1; Page 106-108; 176pp; English.
 CC The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type Cry12I8
 CC endotoxin protein
 CC
 XX
 XX
 SO Sequence 2003 BP; 686 A; 348 C; 392 G; 577 T; 0 U; 0 Other;
 Query Match 11.5%; Score 235.6; DB 6; Length 2003;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
 QY 13 AAAAAATAAATGATGAAATGTTGGATGCTTTACGAATCAACTTAATATGCTTAAT 72
 DB 10 AATTAATCAAAATGAAATGAAATTAATGATGCGACCTCTA---CTTGTATCAAT 66
 QY 73 TGTATCCAAAGTATCCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
 DB 67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGTACAAATATGATTAAT 126
 QY 133 AAGAATGGCTAAATATGTGTGATTCAAATACACATTTATGTGATATACAGATAT 192
 DB 127 AAGATATATTTAAATAATGTCTGGCGGAAATGCTAGTGAATACCTGGTTCA----- 177
 QY 193 TCAAGCCCTGAAGCTGCTTAAGTATGATGATGCTGTTTAAACGGTATTAACAGTAT 252
 DB 178 -----CTGAAATACTTGTAGCGGACAAAGATGCACTAAGCCGCAATTTGATATAGTA 231
 QY 253 GGGACTATATCTTTCAATTTAGGGGTCCTTTGGCAAGTCATCATTTGGAAATATTAAT 312
 DB 232 GGTAAATTAATCAAGTTTAAAGGGGTCATTTGTTGGCGGATGATGATCTTTATAC 291
 QY 313 AGGCTAATAGTATTTTATGGGCAAGGCGCTGA-----TCAATTTGAAGCACTTAATGTT 366
 DB 292 CAATTAATGATATTCGTGCGCTTCAAGGGGAAAGATCAATGCAATTTTATGGA 351
 QY 367 CTGTGTGAAGAGCTTTTAAAGAAAGATAGATCAGGCTAAGAGAAATGCTTTAAG 426
 DB 352 CAAGTAGAAGACTCATTAATCAAAAAATAGCAAGATATGCAAGAAATTAAGCGCTTTG 411

QY 427 GAGCTAGAAAGTTTACAGGAAATTTATGAGACTATATCAAACTAGACTGCAGATGGCTA 486
 DB 412 GAATTAGAAAGATAGTATGATTAATTAACAAATTAATCTAATCGCGCTTGAAAGATGGAA 471
 QY 487 GTTAAACAAGATGATGACAAATGAGGAGGCACTAGT---AAGCAGATGCAATTTGTTGAT 543
 DB 472 GAAATCCAAATGTTTCAAGAGCTTACGAGATGTGCGAAATCGAATTTGAAATCTCGGAT 531
 QY 544 AACTTTTGGAAAGATATGCGCAAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTTA 603
 DB 532 AGTTATTTACCAATATATATGCGATCTTTAGAGTACAAATTTTGAAGTACCATTCCTT 591
 QY 604 CCAATATATGACACAGCCCGCAATTTGCAATTTATTTTAAAGATGCTGATTAATTTT 663
 DB 592 ACTGATATGCAATGCGACCAACCTTCATTTACTGTTTAAAGAACCGGTCAATTTT 651
 QY 664 GGAGCAGCTGGCAATTAAGTATGATGAAATTCGATTAATTAATATACAGACTACAAGGA 723
 DB 652 GGAGAAAGATGGGAGATGTCACCAACTACTATTAATTAATTAATTAATGATGCTCAATGAAA 711
 QY 724 CTGATTAGAAATATTAAGATCATTTGATATTAATTAATTAATTAATTAATTAATTAATTT 783
 DB 712 CTTACTGAGAAATATTTCTGATCAGCTGTAAAGTGTATGAAACGTGTTAGCAAAATTA 771
 QY 784 AATCGCTCAAAATGCTCAAGATTTGGTGAGCTTTAATAGTTTGTATCAATATGACATTA 843
 DB 772 AAGGACAGAGGCTTAACAAATGGGTTGACTTAATCAATTCGTTGAGAAATGACACTG 831
 QY 844 ACAGATTTAGATCTGCAATATTTTCAAACTATGATCCAGTAGATCCATTAAGCA 903
 DB 832 GCGGTTTATGATGTTTTCATTTATTTCCAAATTAATGACACAGCGACGTCATCCAAATGGA 891
 QY 904 GTAAAAACGAAATTCGTAAGGAAAGTTTATACAGATCCAGTAGG 947
 DB 892 ACGAAAGCACACTAACAGGGAAGTATATACAGATCCACTGGG 935
 RESULT 12
 ABR87241
 ID ABR87241 standard; DNA; 2010 BP.
 XX
 XX ABR87241;
 AC
 XX 07-OCT-2002 (first entry)
 DT
 XX
 XX
 DE *Bacillus thuringiensis* Cry12I8-1A truncated gene sequence.
 XX
 XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry12I8; gene; ds.
 XX
 OS *Bacillus thuringiensis*.
 XX
 PN MO200234774-A2.
 PD
 XX
 XX 02-MAY-2002.
 PF 24-OCT-2001; 2001WO-US045468.
 PR 24-OCT-2000; 2000US-0242838P.
 PR 23-OCT-2001; 2001US-00032717.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Abbad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 XX WPI; 2002-519178/55.
 DR P-PSDB; AAU99262.
 XX
 PT New isolated pesticidal polypeptide useful for impacting insect pest e.g.
 XX Colorado potato beetle.
 PS Claim 1; Page 123-125; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type Cry1218
 CC endotoxin protein
 XX
 SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;
 Query Match 11.5%; Score 235.6; DB 6; Length 2010;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
 13 AAAAAATGAATGAATGAATGTTGAGTCTTACGAATCACTGAATATGCTTAAT 72
 10 AATTAATCAAAATGAATGAATGAATTAATGATCGACACTTCTA--CTTCTGATCCAAAT 66
 73 TGTATCAAGATATCACTAGCAAAAAGATCCAAATGACTATGCGAAACGCAACTAT 132
 67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAATATGCGCTACAAATATGATTTAT 126
 133 AAGAAATGGCTAAATATGATGATTCAAATACAAATTAATTTGATATAGACGATAT 192
 127 AAGATTAATTTAAATATGTCGCGGAAATGCTGATGATACCTGTGTTCA----- 177
 193 TCTAGCCCTGAGAGCTCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 252
 178 -----CCTGAAAGTACTGTTAGCGAAGATGATGATGATGATGATGATGATGATGAT 231
 253 GGAAGTACTTACTTGAATTTAGGGGTCCTTTGGCAATGATGATGATGATGATGATGAT 312
 232 GGTAAATTAATCAATGATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGAT 291
 313 AGGCTAAATGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGAT 366
 292 CAATTAATGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGATGAT 351
 367 CTGTTGAAGATGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGAT 426
 352 CAATTAATGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGATGAT 411
 427 GAGCTAAGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGATGAT 486
 412 GAATTAAGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGATGAT 471
 487 GTTAAATGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGATGAT 543
 472 GAATTAATGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGATGAT 531
 544 AACTTTTGAAGATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGATGAT 603
 532 AGTTAATTTAGCAATTTATTTAGGGGTCCTTTGGGCGGATGATGATGATGATGATGAT 591
 604 CCAGTATATGCAAGAGCGGATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTT 663
 592 ACTGTAATGCAATGAGCGGATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTT 651
 664 GGAGCAAGTGGCAATTTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
 652 GGAAGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
 724 CTGATTAAGATTTATTTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
 712 CTTACTGCAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
 784 AATGCTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843

Db 772 AAGGCAAGAGCGGTAAACAATGGTGAATTAACCAATTCGTAGAAATGACACTG 831
 Qy 844 ACAGTATTAATTCGCAATATTTATTTCCAACTATGATGATGATGATGATGATGATGAT 903
 Db 832 GCGGTTTAAATGTTGTTGCTATTTCCAAATTAATTAACACAGCAGTACCAATGGA 891
 Qy 904 GTAAATTAAGATTTAGTGAAGATTTATTAATTAATTAATTAATTAATTAATTAATTA 947
 Db 892 ACAGAAACACACTAACAAGGAAATGATTAATGATGATGATGATGATGATGATGATGAT 935
 RESULT 13
 ADL15314
 ID ADL15314 standard; DNA; 2010 BP.
 AC ADL15314;
 AC ADL15314;
 DT 06-MAY-2004 (first entry)
 XX B thuringiensis strain 1218 Cry1218-1 (Cry8Bb1) truncated DNA.
 DE endotoxin; proteolytic site; insect gut; pesticidal; agriculture;
 KM plant pest; Cry8-like delta-endotoxin; Cry1218-1; Cry8Bb1; ds; gene.
 XX *Bacillus thuringiensis*.
 OS WO2004003148-A2.
 PN 08-JAN-2004.
 PD 25-JUN-2003; 2003WO-US020027.
 PP 26-JUN-2002; 2002US-0391786P.
 XX 04-APR-2003; 2003US-0460787P.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Abad AR, Flanagan RD, Herrmann R, Kahn TW, Lu H, McCutchen BF;
 PI Presnall JK, Wong JFH, Yu C;
 XX WPI; 2004-083033/08.
 DR P-PSDB; ADL15315.
 DR New endotoxin comprising a mutation consisting of the alteration of at
 PT least one proteolytic site, where stability of the endotoxin in insect
 PT gut is increased, useful for providing improved pesticidal activity.
 XX Example 4; SEQ ID NO 11; 333pp; English.
 XX The invention relates to a novel endotoxin having a mutation consisting
 CC of the alteration of at least one proteolytic site, where the stability
 CC of the endotoxin in an insect gut is increased relative to an endotoxin
 CC lacking the mutation. The endotoxin of the invention may be useful for
 CC providing improved pesticidal activity against insect pests whilst the
 CC compositions of the invention may be useful in agriculture for
 CC controlling pests, including plant pests. The current sequence is that of
 CC the DNA related to *Bacillus thuringiensis* strain 1218 Cry8-like delta-
 CC endotoxin Cry1218 of the invention.
 XX
 SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;
 Query Match 11.5%; Score 235.6; DB 12; Length 2010;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
 13 AAAAAATGAATGAATGAATGTTGAGTCTTACGAATCACTGAATATGCTTAAT 72
 10 AATTAATCAAAATGAATGAATGAATTAATGATCGACACTTCTA--CTTCTGATCCAAAT 66
 73 TGTATCAAGATATCACTAGCAAAAAGATCCAAATGACTATGCGAAACGCAACTAT 132
 67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAATATGCGCTACAAATATGATTTAT 126

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QY 133 AAGAAATGCTAAATATGTGTGATTCAAATACAAATTTATGTGTATATTAACAGCTAT 192
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Db 127 AAGATTTATTTAAATATGTCGGGGAAATGTAGTAAATACCTGGTTCA----- 177
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   |||
QY 193 TCTAGCCCTGAACTGCTTTAAGTGTACGAGATGCTGTTTTAAACGGTATTAACAGGTGTA 252
   |||
   |||
   |||
Db 178 -----CTGAAATGACTGTTGTAGCGGCAAGATGCACTTAAGGCCGAATTTGATATAGTA 231
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   |||
   |||
QY 253 GGGACTATATCTTGAATTTAAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAATAGT 312
   |||
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Db 232 GGTAAATTAATCAAGTTTAAAGGGGTCCTTGTGTTGGCCGATAGAGATCTTTATCT 291
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QY 313 AGGCTAATAGATTTTATGAGGCAAGGCGCTGA-----TCCATTTGAAGCACTTAATGTT 366
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Db 292 CAATATTATGATTTCTGTGGCTTCAGGGGAAAGATGCAATGGGAAATTTTATAGAA 351
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QY 367 CTGTGTTGAAGAGCTTATTAAGAAAAGTATGATCAGGTGTAAAGAAAATGCTTTAGA 426
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QY 427 GAGCTAAGAGTTTACAGGGAATATGAGACTATATCAACTAGACTGCAAGATGGCTA 486
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Db 412 GAATTAAGAGATTTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471
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QY 487 GTTAAAGAAATGATGCAATTCGAGGGCACTAGT--AAAGCAATATGCAATTTGAT 543
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   |||
   |||
Db 472 GAAATTCCAATGTTTCAGAGGCTTCAGAGATGTGGAATGCAATTTGAAATCTGAT 531
   |||
   |||
   |||
QY 544 AACTTTTGAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
   |||
   |||
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Db 532 AGTTTATTTAAGCAATATATGCAATCTTTTAAAGTGAATTTTGAAGTACCAATTCCT 591
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QY 604 CCAGTAAATSCAAGAGCGGCAATTTGATTTAATTTTATTAAGAGATGCTGATTTATTT 663
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Db 592 ACTGTATATGCAATGCGAGCAACCTTCAATTTACTGTTATTAAGAGCGGTCAATTTT 651
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QY 664 GGAGCAAGTGGCAATTTAGTGTATGATGAATTCGTATTAATTAATCAGACTACAGGA 723
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Db 652 GGAGAAATAGGGGATGATGCAACAACTACTTAATTAATTAATTAATTAATTAATTA 711
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QY 724 CTGATTAAGAAATTAAGATCAATGTTATTAATTAATTAATTAATTAATTAATTAATTA 783
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Db 712 CTTAAGTCAAGAAATTTCTGATCACTGTGTAAGGTGTAATAAATCTGTTTAAAGAAATTA 771
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QY 784 AATCGCTCAATGCTCAAGATTTGGTGTAGCTTTAATAGTTTGTGTAAGATATGACATTA 843
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QY 844 ACAGTATTAATGATCTCGCAATATTAATTTCAAACTATGATCCAGGTAGATTCATTAACA 903
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Db 892 ACGAAAGCAACAACTAACAGGGAATTAATTAACAGATTCACACTGGG 935
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RESULT 14
 AEB45616
 ID AEB45616 standard; DNA; 2010 BP.

AC AEB45616;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE B. thuringiensis Cry toxin, Cry12Ib-1 (truncated), DNA.
 XX
 KM Toxin; de; gene; transgenic plant; insecticide; pesticide;
 XX plant insect pest; Cry8.
 OS Bacillus thuringiensis; strain 1218-1.
 OS Synthetic.

```

XX PN WO2005066349-A2.
XX PD 21-JUL-2005.
XX PF 09-DEC-2004; 2004MO-US041530.
XX PR 24-DEC-2003; 2003US-00746914.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PT Abad A, Dong H, Herrmann R, Lu A, McCutchen BF, Rice JA;
XX PT Scheper E, Wong YF;
XX DR WPI; 2005-533612/54.
XX DR P-PSDB; AEB45617.
XX PT Novel isolated nucleic acid molecule having nucleotide sequence encoding
XX PT pesticidal polypeptide comprising engineered proteolytic protection site
XX PT resistant to protease, useful for protecting plant from pest e.g.
XX PT Colorado potato beetle.
XX PS Example 4; SEQ ID NO 11; 362bp; English.
XX CC The invention relates to an isolated nucleic acid molecule comprising a
XX CC nucleotide sequence encoding a pesticidal polypeptide having an
XX CC engineered proteolytic protection site, which is not sensitive to the
XX CC plant protease and protects the pesticidal polypeptide from proteolytic
XX CC inactivation in a plant. Also included are protecting (M1) a pesticidal
XX CC polypeptide from proteolytic inactivation in a plant (comprising altering to
XX CC a proteolytic site within the pesticidal polypeptide that is sensitive to
XX CC a plant protease to comprise a proteolytic protection site, where the
XX CC proteolytic protection site is not sensitive to the plant protease and
XX CC protects the pesticidal polypeptide from proteolytic inactivation in a
XX CC plant), an expression cassette (II) comprising the nucleic acid, a
XX CC transformed plant (III) a stably incorporated with the expression
XX CC cassette in its genome, a transformed seed of the plant and an isolated
XX CC pesticidal polypeptide (IV) having proteolytic activity (and comprising
XX CC an engineered proteolytic protection site), which is not sensitive to the
XX CC plant protease and protects the pesticidal polypeptide from proteolytic
XX CC inactivation in a plant). The pesticidal polypeptide is Cry8B1 toxin or
XX CC its variant or fragment, where the variant and the fragment have
XX CC pesticidal activity and the variant has at least 70 % sequence identity
XX CC to an amino acid sequence for the Cry8B1 toxin. The nucleic acid and/or
XX CC expression cassette are useful for protecting a plant from a pest, where
XX CC expression of the nucleic acid and/or expression cassette in the plant
XX CC produces the pesticidal polypeptide in the plant, and where the
XX CC pesticidal polypeptide protects the plant from the pest. The plant
XX CC protease is a cysteine protease. The pest is chosen from Colorado potato
XX CC beetle, Western corn rootworm, Southern corn rootworm, and boll weevil.
XX CC The present sequence encodes a truncated Bacillus thuringiensis Cry8-1like
XX CC toxin, described in the examples section of the specification.
XX SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;

```

Query Match 11.5%; Score 235.6; DB 14; Length 2010;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

QY 13 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 72
   |||
   |||
   |||
Db 10 AATTAATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 66
   |||
   |||
   |||
QY 73 TGTATCAAGATATCACTAGCAAAAGATCCCAATGACTATGCGAAACAGCACTAT 132
   |||
   |||
   |||
Db 67 GATTCTTAACGATATCCCTTTTGGCAATGAGCCCAACAAATGCGTACAAAATATGATAT 126
   |||
   |||
   |||
QY 133 AAGAAATGCTAAATATGTGTGATTCAAATACAAATTTATGTTGATATTAAGCAAGCTAT 192
   |||
   |||
   |||
Db 127 AAGATTTATTTAAATATGTCGGGGAAATGTAGTAAATACCTGGTTCA----- 177
   |||
   |||
   |||
QY 193 TCTAGCCCTGAACTGCTTTAAGTGTACGAGATGCTGTTTAAACGGTATTAACAGGTGTA 252
   |||
   |||
   |||

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Db      178 -----CTGAGACTACTGTTAGCGGACAGATGCGACTAGGCGCGAATTTGATATAGTA 231
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Db      232 GGTAAATTACTATCAGGTTTGGGGTCCCATTTGTTGGCCGATGATGATCTTTATACT 291
Qy      313 AGGCTAATAGTATTTTATGGGCGAGGCGCTGA-----TCCATTTGAGCACTTATGTT 366
Db      292 CAACCTATTGATTTCTGTGCGCTTCAGGGGAAAAGATCAATGGGAAATTTTATAGAA 351
Qy      367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCTGTAAAGAAAATGCTCTTGA 426
Db      352 CAGGTAGAAGACTCTTATTAACAAAATAGCAGAAATATCAAGAAATTAAGGCTTTG 411
Qy      427 GAGCTAGAAGCTTACAGGGAATTAAGACTATATCAACTAGACTGCAAGCATGGCTA 486
Db      412 GAATTAAGAAAGATTAGTAAATTAATTAACCAATTAATCTGCGCTTGAAGAAATGGAA 471
Qy      487 GTTAACAAAGATGATGACAAATCGAGGGCACTAGT---AAGCAGTATGCAATTTGTAT 543
Db      472 GAAATTCCAATGTTTCAAGACCTTAGATGTGGAATGATTTGAAATCTTGAT 531
Qy      544 AACTTTTTCGAAAAGAAATATGCCAAAATTCAGAGAAAAGAACTTTGAAATTTATGTTA 603
Db      532 AGTTTATTTACGCAATATATGCGCATCTTTAGAGTGAACAAATTTTGAATGACATTCCT 591
Qy      604 CCAGTATATGACAAAGCCGCGAATTTGATTTATTTATTAAGATGCTGATATTTT 663
Db      592 ACTGTATATGCAATATGCGACCAACCTTCATTTACTGTTATTAAGAGCGGTCATTTT 651
Qy      664 GGAGCAGTGGCAATTAAGGTATGATGAATTCGTATTAATTAATCAGACTACAAGA 723
Db      652 GGAGAAAGATGGGATGTCAACACTATCTATTAATCTATTTATGCTCAATGAAA 711
Qy      724 CTGATTAAGAAATATTAAGATCAATTTGATTAACAATCTATTAACAAGGTTTAAATCA 783
Db      712 CTTAGCGCAATATTTCTGATCACTGTGTAAGGTATGAAATCTGTTTAGCAAAATTA 771
Qy      784 AATCGCTCAAAATGCTCAAGTTGGGTAGCTTTATATAGTTTGTATCAGATATGACATTA 843
Db      772 AAAGGACGAGCCCTAAACAATGGGTGACTATTAACCAATTCGTAGAGAAATGACACTG 831
Qy      844 ACAGTATTAATCTCGCAATATTTATTCAAACTAGATGCAAGTATGATTCATTAACA 903
Db      832 GCGGTTTATGATGTTGTCATTTATCCCAATTTATACACAGCAGCTACCCAAATGAAA 891
Qy      904 GTAAAAACGGAATTTAGTAGGGAAGTTTATACAGATCCAGTAGG 947
Db      892 ACGAAAGCAACAATAACAAGGAAGTATATACAGATCACTGGG 935

```

RESULT 15

AAT43221
ID AAT43221 standard; DNA; 3507 BP.

AC AAT43221;

DT 16-OCT-2003 (revised)
DT 28-JAN-1997 (first entry)

DE Antiscarab pest toxin 50C(b) coding sequence.

KM Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
KM larval stage insect; grain; tuberous crop; white grub; chafer grub;
KM cyclocephala; popillia; de.

OS Bacillus thuringiensis; strain kumamotoensis.

PN USS554534-A.

PD 10-SEP-1996.

XX

```

Pf      30-SEP-1994; 94US-00315468.
XX
XX 16-DEC-1991; 91US-00808316.
PR 30-JAN-1992; 92US-00828430.
PR 01-FEB-1993; 93US-00014941.
XX
XX (MYCO) MYCOGEN CORP.
XX
XX Fonceirada L, Narva KE, Michaels TE;
XX
XX WPI: 1996-424659/42.
DR P-PSDB; AAM06417.
XX
XX New nucleic acid encoding B. thuringiensis toxin active against scarab(s)
PT - also related toxin and transformed microbes, effective against adult
PT pests and their larvae.
XX
XX Claim 2; Col 27-30; 24pp; English.
XX
XX AAT43221-T43223 represent the coding sequences for toxins that are active
CC against scarab pests. This sequence was isolated from the Bacillus
CC thuringiensis strain kumamotoensis. Insects in the family Scarabaeidae
CC constitute a serious pest control problem, especially when destructive
CC larval stage insects infest high value turf courses,
CC playing fields and lawns. The larvae of many species also attack grains,
CC tuberous crops, and ornamentals. The larvae are known as white grubs, or
CC chafer grubs, and can be found in decaying organic matter, or in the soil
CC where they consume plant roots. In Europe and the U.S. populations of
CC these larvae and adults have developed resistance to chemical
CC insecticides such as the organochlorines and DDT. The toxins encoded by
CC these sequences, and intact cells that are capable of expressing the
CC proteins, can be used to control many pests of the family scarabaeidae,
CC such as species of Cyclocephala, and Popillia. The toxins are active
CC against larvae (present in soil) and against adults. (Updated on 16-OCT-
CC 2003 to standardize OS field)
XX
XX Sequence 3507 BP; 1256 A; 576 C; 732 G; 943 T; 0 U; 0 Other;
SQ

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Query Match 11.5%; Score 235.6; DB 2; Length 3507;

Best Local Similarity 56.5%; Pred. No. 1,8e-44;

Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

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Qy      13 AAAAATAAAATGAATATGAATGATGCTTTACGAATCACTTAATATGCTTAAT 72
Db      10 AATATCAAAATGAATATGAATATATATATAGATGACACCTTCTATCATC---TGTATCAAT 66
Qy      73 TGTATTCGAAGTATCCACTAGCAAAAGATCCCAATGACTATGGAACAAGAACTAT 132
Db      67 GATTTACAGATACCTTTTGGAAATGAGCCAAACAAATGCGCTACAAAATATGATTAAT 126
Qy      133 AAGAAATGGCTAATATATGATGATTCGAATATACAAATTAATGATATTAACAGATAT 192
Db      127 AAAGATTATTTAAAATATGCTGCGGAAA-----TGTATGTAATACCT 171
Qy      193 TCTAGCCCTGAAGCTCTTAAAGTATACAGATGCTGTTTAAACGGGATATTAACAGTGA 252
Db      172 GTTCACTGAGTATTTCTTAAGCAGCAAGATGAGTAAAGCCCAATGATATAGTA 231
Qy      253 GGGACTATATCTTGAATTTAGGGGTCCTTTGGCAAGTCAATCTTTGGAATATAGT 312
Db      232 GGTAAATTACTATCAGGTTTGGGGTCCCATTTGTTGGCCGATGATGATCTTTATACT 291
Qy      313 AGGCTAATAGTATTTTATGGGCG-----AGGCGCTGATCCATTTGAGCACTTATGTT 366
Db      292 CAACCTATTGATTTCTGTGCGCTTCAGGGGAAAAGATCAATGGGAAATTTTATAGAA 351
Qy      367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCTGTAAAGAAAATGCTCTTGA 426
Db      352 CAGGTAGAAGACTCTTATTAACAAAATAGCAGAAATATCAAGAAATTAAGGCTTTG 411
Qy      427 GAGCTAGAAGCTTACAGGGAATTAAGACTATATCAACTAGACTGCAAGCATGGCTA 486
Db      412 GAATTAAGAAAGCTTAGTAAATTAATTAACCAATTAATCTGCGCTTGAAGAAATGGAA 471

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QY	487	GTTAACAAGATGATGACATCGAGGGGCACTAGT---	AACGAGATCAATCTGTTGAT	543
Db	472	GAATAATCCAAATGTTCAAGACCCTTACAGAGATGTTCGAAATCGAATTTGAAATCCTCGAAT		531
QY	544	AACTTTTTCGAAAAGATATGCGCAAAATTCAGAGAAAGAACTTTGAAATTTATTTGTTA		603
Db	532	AGTTATTTTACGCAATATATGCGCATCTTTTCGAGTACAAAATTTTGAAATGACATTCCTT		591
QY	604	CCAGTATATGCAACAAGCCGCGAATTTGCATTTATTTTATTTAAGATGCTGATTTATTTT		663
Db	592	ACAGTATATACATGCGACAGCAAACTCAATTTTCTTTTATTAAGGACGATCAATTTT		651
QY	664	GGAGCACAGTGGCAATTAGTGATGATGAAATTCGTATATATATATACAGACTACAAGGA		723
Db	652	GGAGAAAGATGGGGATGTTGTTCAAGACACTATTTAATTACTATATATGTCGTAATGAAA		711
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Db	712	CTTACTGAGAAATATCTGACCACTGTGTAAAGTGTATGAACAATGTTTAGCAAAATTA		771
QY	784	AATCGCTCAAAATGCTCAAGATTGGGTGAGCTTTAATAGTTTCGTACAGATATGACATTA		843
Db	772	AAAGGCTGAGGGCTTAACATATGATAGTACTATTAACCATTCGTTAGGAAGAAATGACATTG		831
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Db	832	ACGGGTGTAGACGTGTGGTCATTTATTTCCAACTAATGATACAGGTACGTATCACTCGGCA		891
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

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12861.112 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:
10: gb_est10:
11: gb_est11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	61	3.0	1101	10	CNS0039G
C 2	56	2.7	1101	10	CNS0039G
C 3	53.2	2.6	1101	10	CNS0039G
C 4	52.8	2.6	575	9	B2780846
C 5	52.8	2.6	928	10	CNS000DY
C 6	52.6	2.6	844	10	BK139987
C 7	51.6	2.5	1101	10	CNS0182P
C 8	50.8	2.5	1101	10	CNS00E07
C 9	50.6	2.5	856	10	AG544460
C 10	50.4	2.5	707	10	CG403581
C 11	49.4	2.4	1001	10	CNS0155H
C 12	49.2	2.4	657	9	B54873
C 13	49.2	2.4	1110	1	AJ925976
C 14	49	2.4	989	10	CNS02HA4
C 15	48.4	2.4	886	10	CZ239945
C 16	48.4	2.4	889	10	CM973509
C 17	48.2	2.4	1110	10	CM939551
C 18	48	2.3	1085	10	CNS012AK
C 19	47.8	2.3	1146	10	CNS021G2
C 20	47.6	2.3	540	3	BP049165
C 21	47.6	2.3	1101	10	CNS014XJ
C 22	47.2	2.3	806	11	CNS04ABE

C 23	47.2	2.3	888	9	AZ550737
C 24	47.2	2.3	893	9	AZ680121
C 25	47.2	2.3	1134	10	CL110320
C 26	47	2.3	602	10	CZ597892
C 27	47	2.3	976	11	CNS04E5M
C 28	46.8	2.3	471	10	CG807194
C 29	46.8	2.3	602	11	DR70247
C 30	46.8	2.3	670	9	B238480
C 31	46.8	2.3	781	10	BX145762
C 32	46.6	2.3	587	9	BH873429
C 33	46.6	2.3	734	10	CNS01OMP
C 34	46.6	2.3	948	10	AG044370
C 35	46.6	2.3	1101	10	CNS003BD
C 36	46.6	2.3	1201	10	CNS015Z2
C 37	46.4	2.3	594	3	BJ393609
C 38	46.4	2.3	1101	10	CNS00E07
C 39	46.4	2.3	1101	10	CNS0106X
C 40	46.2	2.3	641	9	AQ946120
C 41	46.2	2.3	1101	10	CNS016LT
C 42	46	2.2	1101	10	CNS00FVE
C 43	45.8	2.2	506	3	BM276457
C 44	45.8	2.2	536	3	BM275822
C 45	45.8	2.2	764	6	CA856291

ALIGNMENTS

RESULT 1
CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
AL063921 GI:4941778
VERSION
AL063921.1 GI:4941778
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Ooeawa and Aaron Mammoeer in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Source
1. 1101
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/clone_1ib="RPCI-98"
/note="end : TET3"

ORIGIN

RESULT 3
CNS017KE/c 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN37F11 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108152
VERSION AL108152.1 GI:5628456
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLES Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BF 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES
source Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37F11"
/clone_1b="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN
Query Match 2.6%; Score 53.2; DB 10; Length 1101;
Best Local Similarity 35.1%; Pred. No. 0.11;
Matches 184; Conservative 73; Mismatches 258; Indels 9; Gaps 1;
QY 926 AAGTTATACAGATCCAGTGGGTTTACTGGGGTATTGAAAGGAGTGAAGCTTACC 985
DB 651 AAKKAAGKTAACACACAKAAAAAGDCKKGGKDAAPAAKAAKAAKAKKAKK 592
QY 986 CTGTGTAATATCTTAATATACCACTTACTGCTATGAAATTAACGCAAGCAGTC 1045
DB 591 KKAAGKAAAKKDKRAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 532
QY 1046 CTTCCTATACCACTTGGCTTAATCGTATTTTGTATATACAGAGCTTAGTAA---- 1100
DB 531 TTGKWCAGKATTAAGAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 472
QY 1101 -----TATGTCGATGCAAAATTTGGGGAGGCGCTACATAGTTGAAATGGAATG 1156
DB 471 ATTAAATGTTTTGTTATTTATTTTATTTTATTTATTTATTTATTTATTTAA 412
QY 1157 ATGGTCTGAATTAACCATTAACCTTGGTAAACGATGATCTATTAATCTCAATATT 1216
DB 411 ATTATTTGAATTAATAAGTATTTTATTTATTTATTTATTTATTTATTTAAKMA 352
QY 1217 TTAATTTGGGAACCTTTCTGTTTCAGATGATGATCACTGCTGATATATTTAGAG 1276
DB 351 WMAWMAWMTTAAWAAATTAATTTATTTTAAAGTTTATTTTATTTTATTTAT 292
QY 1277 GAACAGAGGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1336
DB 291 AAATTT 232
QY 1337 CATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1396

RESULT 4
BZ780846 575 bp DNA linear GSS 14-MAR-2003
LOCUS BZ780846
DEFINITION 1120h11.g1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor
ACCESSION BZ780846
VERSION BZ780846.1 GI:28958388
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 575)
REFERENCE Rabinowitz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zlatavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
JOURNAL Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: 1120 row: h column: 11
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 575.
FEATURES
source Location/Qualifiers
1..575
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="1120h11"
/lab_host="DH5a"
/clone_1b="WGS-SbicolorF (DH5a methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I and one nucleotide was added by fill in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (Xba I/Xba I reads in M13mp19, into DH5a.."

ORIGIN
Query Match 2.6%; Score 52.8; DB 9; Length 575;
Best Local Similarity 46.7%; Pred. No. 0.12;
Matches 168; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 992 ATATATCTTAATTAATCAACTTACTGCTATGAAATTAACGACGAGCTCTTCT 1051
DB 198 ATATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 257
QY 1052 ATACACTTGGCTTAATCGTATTTTGTATATCAAGAGCTTAGGTATATGTCGATG 1111
DB 258 ATATATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 317
QY 1112 TGAGAAATATTTGGGAGGCGACATTAATGTTGAATGATGCTTGAATTA 1171
DB 318 ATATATATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 377
QY 1172 CCATTAACCTTGGTAAACGATTTCTATTAATCTCAATTAATTAATTTGCGAAC 1231

Db 378 ATAAATATCTAATCTAATTAATTAATCTAATATATATCTAATTAATAGTAAATTA 437
QY 1232 TTTCCTGTTTCAGTATAGTCACTGCTGCTATATATTTAGAGGAAGAGGCTAATA 1291
Db 438 CTATATATATATATCTAATTAATTAATATAGTATATATAGTAAATTAATAGTAA 497
QY 1292 ATATATATCTAATCTAATGAGTCTGAGAGTATATTTTAAATACATCAATATTAATA 1351
Db 498 ATATATGATAGTAAATTAATCTAATTAATATATCTAATTAATCTAATTAATCTA 557

RESULT 5
CNS00DKY 928 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR7A24 of RCT-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL071865 GI:4948170
VERSION AL071865.1
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 928)
AUTHORS Genoscope.
TITLE Direct Submision
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqrel@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RCT-98 and was constructed by partial
BclRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1..928
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR7A24"
/clone_1kb="RCT-98"
/note="end : T7"

ORIGIN
Query Match 2.6%; Score 52.8; DB 10; Length 928;
Best Local Similarity 28.6%; Pred. No. 0.14;
Matches 108; Conservative 90; Mismatches 180; Indels 0; Gaps 0;

QY 1161 TTCTGAATTAACCATTAACCTTGGTAAACATGATCTATTAATCTCAATTAATTTTAA 1220
Db 479 WTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 538
QY 1221 TTTCGGCAACCTTCTGTTTTCAGTATAGTCACTGCTCGATATATTTAGAGGAAC 1280
Db 539 WTTTTTAAATTAATTAATTTTATTTTATTTTAAATTTTAAATTTTAAATTAATTA 598
QY 1281 AGAGGCTAAATTAATTAATTTCTAGTCAATGAGTCTGAGAGTATTTTATATCATC 1340
Db 599 AWAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 658

QY 1341 AAATATTAATTAATGTAACCTGATCTTTAAGATACGAAGCGCTGCTATCTTCATCCCA 1400
Db 659 AAAAAAAAAAAAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 718
QY 1401 AACTATATTAATGAGATTAACGAGAAAGATAGCAAGCAACCAAGCAGGATTTGAG 1460
Db 719 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 778
QY 1461 CCATGATTAATCTTATTAATTAATTAATTTGATGACGCGAAGTAGTTCAGCGGATG 1520
Db 779 WW 838
QY 1521 TAGCTTTTAACGTTTGG 1538
Db 839 KKKKBGKKTKTKTKTKG 856

RESULT 6
BX139987 844 bp DNA linear GSS 13-MAR-2003
LOCUS BX139987
DEFINITION Dario rerio genomic clone DKEX-99E7, genomic survey sequence.
ACCESSION BX139987
VERSION BX139987.1 GI:27971314
KEYWORDS GSS.
SOURCE Dario rerio (zebrafish)
ORGANISM Dario rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 844)
AUTHORS Humphrey,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submision
JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humfrey@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 99E7. 99E7 is
part of the Daniokey BAC library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
1..844
Location/Qualifiers
/organism="Dario rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-99E7"
/issue_type="Testis"
/note="Vector pIndigoBAC-536"

ORIGIN
Query Match 2.6%; Score 52.6; DB 10; Length 844;
Best Local Similarity 46.6%; Pred. No. 0.15;
Matches 169; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 992 ATTAATCTTAATTAATTAACACTTACGCTATGGAATAATTAACGACGACGCTTCTT 1051
Db 441 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTG 500
QY 1052 ATACCACTTGGCTTAATCTGATTTTGTATATACAGACTCTAGCTAATATCTGATG 1111
Db 501 ATTAATTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGATA 560
QY 1112 TGAATAATTTGGGAGGACATTAATGTTGAAAAATGAAATGATGTTCTGAATAA 1171
Db 561 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATGATA 620
QY 1172 CCATTAACCTTGGTAAACATGATCTATTAATCTTAATTAATTTTATTTTGGGCAAC 1231
Db 621 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 680
QY 1232 TTTCCTGTTTCAGTATAGTCACTGCTGATATATTTAGAGGAAGAGGCTAATA 1291
Db 681 ATTAATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 740

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Qy 1292 ATTATATTAAGTCAAGTGAAGTCTCGAGAGTATTTTAAATACATCAATATATAA 1351
Db 741 ATATATATATATGATATATATATATATATATATATATATATATATATATATAT 800
Qy 1352 ATG 1354
Db 801 ATG 803

RESULT 7
CNS0182P 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN37D10 of Drosophila library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL108811
VERSION AL108811.1 GI:5629115
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobac11.
FEATURES
source 1..1101
location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37D10"
/clone_1ib="DrosBAC"
/plasmid="pBelobac11"
/note="end : SP6"

ORIGIN
Query Match 2.5%; Score 51.6; DB 10; Length 1101;
Best local Similarity 20.5%; Pred. No. 0.27;
Matches 117; Conservative 209; Mismatches 241; Indels 5; Gaps 1;

Qy 408 AAGAGAAATGCTCTTAGAGAGTAAAGGTTTACAGGGAATTATGACTATATCAAC 467
Db 531 AAAAAAAMAAAAAGKAGAGGRRBVGAGGDAATAAATAAADAADPTKMDAR 590
Qy 468 TAGACGCAAGCATGCTAGTAAAGATGATGACAATCGAGGCACTAGTAACGA 527
Db 591 GAAARAAAAADAARAAAKWTMAAAAAAAGTTTAAATAAAGG 650
Qy 528 GTATGCAATGTTGATTAATTTTCGAAAAAGATATGCAAAATTCAGAGAAAGAACTT 587
Db 651 GAKGTGKRAADDGGAADAWRRGRGRRAAARAAAAAADAARAAAAA 710
Qy 588 TGAATTTTATTTGTAACAGTATATGCAAGCCGCAATTCGATTTAATTTAAG 647
Db 711 AAAADAGRRKWKKGKGGKATKTAAMAKGRKMDWTATATMTWDTWKAATD 770
Qy 648 AGATGCTGATATTTTGCAGACAGTGCATTAAGTGAATGAATGATGATATTA 707
Db 771 AKRAAAGRRRRDKRTARADGRRARRRRRAAAGKARAGARRAR- - -ARRAADR 825
Qy 708 TATCAACTACAGAGCTGATTAGAGAAATTAAGATCATTTGATTAACATTCTATAACA 767

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Db 826 DWDMAAAAAAAMWTTWRDWWDDWTRWDDTTAAWMDARARRRRRR 885
Qy 768 GGGTTAAATCAATTAATGCTCAATGCTCAAGATGGCTTATAGTTTCG 827
Db 886 RRRRRARRAADDTDTKDRMADATTDKDTTWTDDDDWAKARBRMAAKAGAMK 945
Qy 828 TACAGATATGACATTAACAGTATTAATCTCGCAATATATTTTCAAACTATGATCCAGC 887
Db 946 WRDARDDMAATAKDDGDKWKGKRGKDKKDKKDKTKDDDDDKTTRDMMW 1005
Qy 888 TAGTATCCATTGCGAGTAAAAACGAATGACTAGGAAATTTATACAGATCCAGAG 947
Db 1006 WMTRTMDWMDGRRGRWTRRRWGAWMAADMDTDGKDTRTADKDKRTDTTKRD 1065
Qy 948 GTTACTGGGGGTATTAAGAAAGTGAAGTAGGA 979
Db 1066 GDDWRKDKDKKRRDKKDDTKKDATWDDDD 1097

RESULT 8
CNS00E07 1101 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TBT3 end of BAC:
DEFINITION BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069440
VERSION AL069440.1 GI:4949583
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Oosawa and
Aron Memmose in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp. the same strain used for the library
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source 1..1101
location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29P01"
/clone_1ib="RPCI-98"
/note="end : TBT3"

ORIGIN
Query Match 2.5%; Score 50.8; DB 10; Length 1101;
Best local Similarity 36.8%; Pred. No. 0.43;
Matches 119; Conservative 45; Mismatches 159; Indels 0; Gaps 0;

Qy 529 TATGCAATGTTGATTAATTTTCGAAAAAGATATGCAAAATTCAGAGAAAGAACTT 588
Db 569 WATATAAAAAAMATTTTAAATTTTAAATTAATTAATTAAGWMAAADAAMWMTATAMHT 628

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QY 589 GAAATTTTATGTTACAGATATGCAACAGCCGCAATTTGCATTTAATTTATTAGA 648
 DB 629 WTAAATTTTATATMTATTTTAAATATMTATTTTAAATATMTATTTTAAATMTAA 688
 QY 649 GATGCGATTTATTTTGAGACAGGTGCAATTTAGTGATGATCAATTTGCTGATTAAT 708
 DB 689 TATTAARWAAATTTWAAAAAAWAAATTTWAAATTAATAATTTTATTTATTTT 748
 QY 709 ATCAGACATCAAGACATGATTTAGAGATATTAAGATCATTTGATTAACATTTAACCAG 768
 DB 749 AAMWATTTAAATATMTATMTATMTAAWATTTWAAAAAAATMTATTAATAATTTWKATA 808
 QY 769 GGTTTAAATCAATTTAATGCTCAAAATGCTCAAGATTTGGTGAGCTTTAATAGCTTT 828
 DB 809 TWTATWMTTTTAAATATMTATTTTAAATTTTATTTTATTTTATTTTAAATTTT 868
 QY 829 ACAGATATGACATTTACAGATTT 851
 DB 869 WWTAAWAWGTATTAATWAAATTTAAW 891

RESULT 9

AG544460/c 856 bp DNA linear GSS 23-DEC-2004
 LOCUS Mus musculus molossinus DNA, clone:MSMg01-458L01.T7, genomic survey
 DEFINITION sequence.
 ACCESSION AG544460
 VERSION AG544460.1 GI:48304874

KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus

REFERENCE 1 Abe, K., Noguchi, H., Tagawa, K., Yuzurika, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwa, K., and Shiroishi, T.
 Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)

REFERENCE

AUTHORS

TITLE

JOURNAL PUBLISHED
 REFERENCE 2 (bases 1 to 856)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenhiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

JOURNAL

AUTHORS

COMMENT Clones are derived from the mouse BAC library MSMG01. For BAC library availability, please contact Kuniya Abe (abe@rc.riken.jp).
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Tsukuba Institute, Bio Resource Center,
 Tsukuba, Ibaraki, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rc.riken.jp

COMMENT

PRIMERS
 Sequencing : T7
 LIBRARY : PBACg3.6
 Vector : EcoRI
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI

FEATURES

source

Location/Qualifiers
 1..856
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-458L01.T7"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"

ORIGIN

/clone_1ib="MSMg01 Mouse Male BAC Library"

Query Match 2.5%; Score 50.6; DB 10; Length 856;
 Best Local Similarity 47.8%; Pred. No. 0.46;
 Matches 140; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 550 TTGGAAGAAATATGCGCAAAATTCAGAGAAAGAACTTTGAATTTATTTTACAGTA 609
 DB 821 TTGGAAGAAATATGCGCAAAATTCAGAGAAAGAACTTTGAATTTATTTTAAATA 762
 QY 610 TATGCAAGCCGCAATTTGATTTAATTTATTTAAGAGATGCTATTTATTTTGAGCA 669
 DB 761 TTTTGTAAAAATGTTNGGTTATTAATAATTTGATTAATAATTTTAAAAATTAATA 702
 QY 670 CAGTGCAATTTAGTGATGATGAAATTCGTAATTTATATACACTAACAGAGATGATT 729
 DB 701 AATTNTATATATNTTAAATTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTA 642
 QY 730 AGAGATATTAAGATCATTTGATTAACATTTCTAATTAACAGGTTTAATCAATTTAATCGC 789
 DB 641 TATTTTATTAATAATATATTAATAATTAATATATATATATATATATATATATATAT 582
 QY 790 TCAATGCTCAAGATTTGGGTGAGCTTTAATAGCTTCGTACAGATATGACATT 842
 DB 581 AAAAAATTTTATGAATAATATTTGTTTAATTAATTAATTAATTAATTAATTAAT 529

RESULT 10

CG403581 707 bp DNA linear GSS 02-SEP-2003
 LOCUS ZMMBBb0248A07.r ZMMBBb Zea mays genomic clone ZMMBBb0248A07 3',
 DEFINITION genomic survey sequence.
 ACCESSION CG403581
 VERSION CG403581.1 GI:34402465

KEYWORDS

GSS.

SOURCE

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

REFERENCE

AUTHORS Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J., and Wing, R.
 Sequencing of the maize genome
 Unpublished (2003)

TITLE

JOURNAL

CONTACT: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3667

Fax: 520 621 9288

Email: twing@genome.arizona.edu

PCR Primers

FORWARD: T7

BACKWARD: M13r

Plate: 0248

row: A

column: 07

Seq primer: M13r

Classes: BAC ends.

Location/Qualifiers

1..707

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="ZMMBBb0248A07"

/lab_host="DH10B"

/clone_1ib="ZMMBBb"

/note="Vector: pBelBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"

HindIII; Zea mays L. ssp. mays"

HindIII; Zea mays L. ssp. mays"

HindIII; Zea mays L. ssp. mays"

HindIII; Zea mays L. ssp. mays"

HindIII; Zea mays L. ssp. mays"

FEATURES

source

Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBBb0248A07"
 /lab_host="DH10B"
 /clone_1ib="ZMMBBb"
 /note="Vector: pBelBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 2.5%; Score 50.4; DB 10; Length 707;
 Best Local Similarity 46.0%; Pred. No. 0.49;
 Matches 171; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 982 TACCCTGGATATACCTATATACACCTTACTGCTATGAGAAATACGACGCA 1041
 |||||
 DB 216 TACCCATGGATATATATATATATATATATATATATATATATATATAT 275
 QY 1042 CGTCTTCTATACCACTGGCTTAATCGATTTTGTATATACAAGACTAGTAAT 1101
 |||||
 DB 276 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 335
 QY 1102 ATGCTGATGTGAAATATTTGGGAGGCGATACATTAGTGAATGAAATGATGT 1161
 |||||
 DB 336 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 395
 QY 1162 TCGAATTAACCATTAACCTTGGTAAACGATTCCTTACTCTATTCATATTTTAA 1221
 |||||
 DB 396 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 455
 QY 1222 TTGCGAACCTTCTGTTTTCAGTATGAGTCACTGCTGATATATTAAGAGGACA 1281
 |||||
 DB 456 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 515
 QY 1282 GAGGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1341
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 DB 516 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 575
 QY 1342 AATTAATTAAT 1353
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 DB 576 AATTAATTAAT 587

RESULT 11
 CNS0155H 1001 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
 DEFINITION BACN13C23 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL105023 GI:5617037
 VERSION GSS.
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1001)
 Genoscope.
 REFERENCE Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 AUTHORS BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 JOURNAL - Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billand at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES
 source Location/Qualifiers

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 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACN13C23"
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 /plasmid="pBelobAC11"
 /note="end : SP6"

ORIGIN
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Best Local Similarity 32.8%; Pred. No. 0.92;
 Matches 141; Conservative 81; Mismatches 207; Indels 1; Gaps 1;

QY 376 GAGCTTATTAAGAAAGTATATAGATCAGCGTGTAGAGAAAATGCTCTTACAGCTGAA 435
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 DB 536 GAGTAANWRRAAAGCAAAAGRRVARKWGDAGAGAADAGAAATANAGAAAAGKRGMA 595
 QY 436 GGTTCAGGGAATTAAGACATATATCAAACTAGACTGCAACATGCTAGTTAACAG 495
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 DB 596 AABDAGRASAAAKTKTGARAGAAAAGWDADATWTKXBARAKADADWAAAAACA 655
 QY 496 AATGATGACATCGAGGCGCATATGTRAGCACTATGCAATTTGTTAACTTTTGAA 555
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 DB 656 AAANVHAAMAAARAGRAARRRAAAAARADARAAAARAAARARARAAAATAA 715
 QY 556 AAGATATGCGCAATTCAGAAAGAACT-TTGAATTTTATTTGTTACAGATATGC 614
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 DB 716 AAWAATTAARAAARARARARARARARARARARARARARARARARARARAR 775
 QY 615 ACAAGCCGCAATTCATTTAATTTATTAAGAGATGCTGATATTTTGGACACAGTG 674
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 DB 776 WAAATTAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAAATTAATA 835
 QY 675 GCAATTAAGTATGATGAATTTGCTGATATTTATCAGACTCAAGGACTGTTAGAGA 734
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 DB 836 AAAAAATTAATTTTAAAAAAMAAWMAATMAATTAATAADAAAAAAMAAWATA 895
 QY 735 ATTAAGAATCATTTGATATATCATTTAATACGAGGTTTAATCAATTAATGCTCAA 794
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 DB 896 AATTAATAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 955
 QY 795 TGCTCAAGAT 804
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 DB 956 WATTAATAAT 965

RESULT 12
 B54873 657 bp DNA linear GSS 20-JUN-1998
 LOCUS CIT-HSP-384M15.TF CIT-HSP Homo sapiens genomic clone 384M15,
 DEFINITION genomic survey sequence.

ACCESSION B54873 GI:2609207
 VERSION GSS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE Adams M.D., Rounsley S.D., Field C.E., Bass S., Linher K.,
 AUTHORS Golden K., Berry K., Granger D., Suh E., Mible C., Shinya H.,
 TITLE Simon M. and Venter V.C.
 JOURNAL Use of a random BAC End Sequence Database for Sequence-Ready Map
 COMMENT Unpublished (1997)
 Building
 Other GSSs: CIT-HSP-384M15.TR
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source Location/Qualifiers

1..657
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/db_xref="GDB:5378461"
/db_xref="taxon:9606"
/clone="384M15"
/sex="Male"
/cell_type="Sperm"
/clone_1ib="CIT-HSP"
/note="Vector: pBelOAC11, Site_1: HindIII; Site_2:
HindIII"

ORIGIN

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Best Local Similarity 46.3%; Pred. No. 0.95;
Matches 162; Conservative 0; Mismatches 188; Indels 0; Gaps 0;
QY 1047 TCTCTTACACCTGGCTTATCGTATTTTGTATATACAGAGCTAGATATATGTC 1106
DB 126 TTTATATATATATGATATATATATATATATATATATATATATATATATATAT 185
QY 1107 TGAATGAGAAATATTTGGGAGGCGATACATTAGTTGAAATGGAATGATGTTCTGA 1166
DB 186 TATATATGAT 245
QY 1167 AATPACCATTAACCTTGGTAAACGATCTATATACCTCATCAATATTTTAATTCGC 1226
DB 246 TATATTTTATATATATATATATGTTATATATATATATATATATATATATATATAT 305
QY 1227 GAACCTTTCGTTTGTAGTATGATGCTGCTCGTATATATTTTGAAGAGACAGAGGC 1286
DB 306 TAT 355
QY 1287 TATATATATATATATAGTATGATGAGTCTCGAGATTTTGAATCAATCAATAT 1346
DB 366 TAT 425
QY 1347 AATATATGACCTGATCTTAAAGATACGAAGCCCTGCAATCTTCAT 1396
DB 426 ATATATATGAT 475

RESULT 13
AJ925976 1110 bp mRNA linear EST 10-JUN-2005
LOCUS AJ925976 Theileria annulata merozoite Theileria annulata cDNA clone
DEFINITION csm009h03_g1k, mRNA sequence.
ACCESSION AJ925976
VERSION AJ925976.1 GI:67496349
KEYWORDS EST.
SOURCE Theileria annulata
ORGANISM Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
Theileria.

REFERENCE 1 (bases 1 to 1110)
Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
Kerhoulou,A., Aslett,M., Bishop,R., Boucquier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Laird,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,F.,
Nene,V., O'Neill,S., Price,C., Quail,M.A., Rabinowitsch,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,F.,
Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J.,
Dobbelaeere,D.A.E., Langsley,G., Rajandream,M.-A., McKeever,D.,
Shiels,B., Tait,A., Barrall,B. and Hall,N.
The genome of a host-cell transforming parasite Theileria
annulata and a comparison with T. parva
Unpublished (2005)
JOURNAL Contact: Pain A
COMMENT The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Camps, CB10 1SA, UNITED KINGDOM
Merozoite cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
location/Qualifiers
1. .1110

FEATURES
source

/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="csm009h03_g1k"
/dev_stage="merozoite"
/lab_host="Bos taurus (cow)"
/clone_1ib="Theileria annulata merozoite"
/note="country: Turkey; Ankara"

ORIGIN

Query Match 2.4%; Score 49.2; DB 1; Length 1110;
Best Local Similarity 29.8%; Pred. No. 1;
Matches 108; Conservative 0; Mismatches 254; Indels 0; Gaps 0;
QY 389 AAGATATAGATACGCGTGAAGAAAATGCTCTTATAGAGCTAGAAGGTTTACAGGAA 448
DB 710 AA 769
QY 449 TTAAGACTATATCAAACTAGACCTGCAAGCATGCGTATTAACAAGATGATGACAATC 508
DB 770 NTANANANANNNNNNAAAAATTAANANNNNTNANANANNNNANANANNNNNNTA 829
QY 509 GGAAGGCACTAGTAAGCGATGCAATGTTGATTAACCTTTTCGAAAAGATATGCCA 568
DB 830 NNNNNNTTTNNNANNA 889
QY 569 AATTCAGAGAAAGAACTTGAATTTTATTTGTTACAGATATGCAAGCCGCAATT 628
DB 890 NNNANNNNTTANNNNNNTNNNTTNTTNTTNTTNTATTAATTAATNTATNTATNTAT 949
QY 629 TGCATTTAATTTTATTAAGATGCTGATTTTGGAGACAGTGGCAATTAGTGATG 688
DB 950 TATTAAGTTATTTTAAATATATTAATAANAAAAATTTAATATNTTNTATNTATATA 1009
QY 689 ATGAATTTGATATATTTATATCAAGCTACAGACTGATTAGAAATTAAGATCAT 748
DB 1010 NNNAAATTAATGNNAAAAATNTAATNTAATTAATTTATAGATGATTAATGATTAAN 1069
QY 749 GT 750
DB 1070 NT 1071

RESULT 14
CNS02HA4 989 bp DNA linear GSS 01-SEP-2000
LOCUS CNS02HA4
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
139021 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL197365
VERSION AL197365.1 GI:7835515
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE 1
Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizmes,C., Wincker,P., Brotilier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL 10835645
PUBMED 2
REFERENCES
Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Coataz,C.,
Fizmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis

TITILE

TITILE

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 13:22:10 ; Search time 391 Seconds

(without alignments)
9315.150 Million cell updates/sec

Title: US-10-782-096-1

Sequence: 1 atgaattcataaataaa.....atgattattatcaatcaa 2049

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents NA:*

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8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.2	12.5	3471	2 US-07-876-280-29	Sequence 29, Appl
2	256.2	12.5	3471	2 US-07-812-180A-1	Sequence 1, Appl
3	256.2	12.5	3471	2 US-08-315-468-1	Sequence 1, Appl
4	256.2	12.5	3471	3 US-07-941-650A-1	Sequence 1, Appl
5	236	11.5	3504	3 US-10-089-678-2	Sequence 2, Appl
6	236	11.5	3690	3 US-10-089-678-3	Sequence 3, Appl
7	235.6	11.5	3507	2 US-08-315-468-3	Sequence 3, Appl
8	231	11.3	1607	3 US-08-286-870A-5	Sequence 5, Appl
9	231	11.3	1946	3 US-08-286-870A-3	Sequence 3, Appl
10	229.4	11.2	2965	3 US-08-460-570-1	Sequence 1, Appl
11	229.4	11.2	2965	2 US-08-460-570-2	Sequence 1, Appl
12	229.4	11.2	2965	3 US-08-286-870A-1	Sequence 1, Appl
13	229.4	11.2	2965	2 US-08-286-870A-2	Sequence 2, Appl
14	223.6	10.9	3684	2 US-08-448-170-7	Sequence 7, Appl
15	223.6	10.9	3684	3 US-08-961-803-5	Sequence 5, Appl
16	223.6	10.9	3684	3 US-09-661-322A-62	Sequence 62, Appl
17	220	10.7	2133	3 US-09-661-322A-41	Sequence 41, Appl
18	216.4	10.6	3797	2 US-07-915-203-1	Sequence 1, Appl
19	216.4	10.6	3797	2 US-08-272-887-1	Sequence 1, Appl
20	216.4	10.6	3797	2 US-08-789-449-1	Sequence 1, Appl
21	209.6	10.2	4074	2 US-08-377-590-1	Sequence 1, Appl
22	207.8	10.1	3471	3 US-09-002-285-73	Sequence 73, Appl
23	207.8	10.1	3471	3 US-09-589-477-73	Sequence 73, Appl
24	207.8	10.1	3471	3 US-09-661-322A-27	Sequence 27, Appl

25	207.8	10.1	3471	3 US-10-099-285A-73	Sequence 73, Appl
26	207.8	10.1	4344	2 US-08-532-547-4	Sequence 4, Appl
27	207.8	10.1	4344	2 US-08-379-656B-4	Sequence 4, Appl
28	207.8	10.1	4344	3 US-08-455-838-4	Sequence 4, Appl
29	207.8	10.1	4344	3 US-09-019-809-4	Sequence 4, Appl
30	207.8	10.1	4344	3 US-09-471-177-4	Sequence 4, Appl
31	207.8	10.1	4344	3 US-09-220-806-4	Sequence 4, Appl
32	206.8	10.1	1561	2 US-08-532-547-2	Sequence 2, Appl
33	206.8	10.1	1561	2 US-08-379-656B-2	Sequence 2, Appl
34	206.8	10.1	1561	3 US-08-455-838-2	Sequence 2, Appl
35	206.8	10.1	1561	3 US-09-019-809-2	Sequence 2, Appl
36	206.8	10.1	1561	3 US-09-471-177-2	Sequence 2, Appl
37	206.8	10.1	1561	3 US-09-220-806-2	Sequence 2, Appl
38	204.6	10.0	4173	3 US-09-661-322A-37	Sequence 37, Appl
39	204.4	10.0	3414	2 US-07-973-320-3	Sequence 3, Appl
40	204	10.0	2180	2 US-09-003-217-1	Sequence 1, Appl
41	203.2	9.9	1464	2 US-08-448-170-9	Sequence 9, Appl
42	203.2	9.9	1464	3 US-08-961-803-6	Sequence 6, Appl
43	201.2	9.8	3414	2 US-07-973-320-1	Sequence 1, Appl
44	201	9.8	1629	6 PCT-US91-02560-3	Sequence 3, Appl
45	200.8	9.8	1897	3 US-09-363-970-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-07-876-280-29
Sequence 29, Application US/07876280
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 52621581 Bacillus thuringiensis Isolates for
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: Controlling Acarides
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C

IMMEDIATE SOURCE: CLONE: E. COLL NM522 (PMYC2320) NRRL B-18769
US-07-876-280-29

Query Match	12.5%	Score 256.2	DB 2	Length 3471
Best Local Similarity	50.5%	Pred. No. 9.5e-53		
Matches 838; Conservative	0	Mismatches 778;	Indels 45;	Gaps 7

Qy	13	AAAAATAAAAATGAATATGAATATGGATGCTTTACAAATCAACTCTAAATATGCTAAT	72
Db	10	AATATACAAATGAATATGAATATTAATGATGACACTTCTAATC---TGATCCAGT	66
Qy	73	TGTTATCCAGATATCCATGACAAAGATCCAAATGACTATGCGAAACGAACTAT	132
Db	67	GATCTCAACAGATACCCCTTTTGCAATGAGCCACAGATGGTTACAAAATATGAATATAT	126
Qy	133	AAAGAAATGGCAAAATATGTGTGATTCAAATACAAATTTATGTGTGATATATAGACCGAT	192
Db	127	AAAGATTAATCGAAAAATGCTGGG-----GGAGAAATCTGAAATTA	168
Qy	193	TCATGACCCCTGAGCTGCTTTAAGTATGACGATGCTGTTTTAAGCGGTATTAACAGTGA	252
Db	169	TTTGGAAATCCGGAGACGTTATTAATGATCATCCACGATTCAAACTGGAATTTGGCATTTGTT	228
Qy	253	GGGACTATACTTTCGAATTTAGGGGTCCCTTTGGCACTCAATCATTTGGAATTAATGT	312
Db	229	GGTCGAATACTAGGAGCTTTTAGGGGTTCCAATTTGCTACTGATAGCTAGTTCATATGT	288
Qy	313	AGGCTAATPAGGTAATTTTATGGGACAG-----GGCGTATCCATTTGAAGCATTAATGGTT	366
Db	289	TTCAATTTGGTCAATTAATGGCCGTCAAAGACGTAGTATATGGGAGAAATTAATGGAA	348
Qy	367	CTTGTGGAAGCTTAATTAAGAAAAATATAGATCAGCGCTGTAGAGAAAAATGCTCTTGA	426
Db	349	CGAGTGAAGAACTCGTTGATCAAAAAATATGAAAAATATGTAAGAAATPAGGCTTTGCT	408
Qy	427	GAGCTAGAAGTTTACAGGGAATTAATGACTATATCAAACCTAGCTGCAAGCATGGCTA	486
Db	409	GAATTTAAAGGGCTAGGAAATGCTTTGGATGTATATACGACATCACTTGAAGATTTGGCTG	468
Qy	487	GTTTAACAAGATGATG--ACAATCCGAGGGGCACTAGTAAGCAGATATGCAATTTGAT	543
Db	469	GAANAATCGCAATGATGCAAGAACTAGAAATGTTGTTCTTAATCAATTTATATAGCTTTAGAT	528
Qy	544	AACTTTTTCGAAAAGAATATGCCAAAAATTCAGGAAAGAAACTTTGAATTTTATTTGTTA	603
Db	529	CTTAACCTTTGTATGTTCAATTCATCTTTTGCAGATATCGGACAGAAATGCTATTAATTA	588
Qy	604	CCAGTATATATGCAACAAGCCGCGCAATTTGCAATTAATTTATTAAGAGATGCTGATTAATTTT	663
Db	589	GCAGTATATATGCAAGCGCTGTGAACCTACATTTATTTATTAAGAGATGCTCTTAATTTT	648
Qy	664	GGAGCAGATGGGCAATTAAGTATGATGAATGAATTTGCTGATTTATTAATCACTCAAGGA	723
Db	649	GGAGAAAGTGGGAAATTTACACAGGTGAAATTTCTAGATTTTATTAATCGTCAAGTGCA	708
Qy	724	CTGATTAAGAAATTAAGATCATTTGATTAACATTTCTATTAACCAAGGTTTAAATCAATTT	783
Db	709	CTTAACCGCTGAATATTCAGACTAATTTGTGTAAAGGTATTAATAATCCGCTTAGATTAATTTG	768
Qy	784	AATCGCTCAAAATGCTCAAGATTTGGGTAGCTTTAATAGTTTCTGTAACGATATGACATTA	843
Db	769	AAAGGTACCACTTCTTAAAGTTGGCTGATTAATCATCGTTCGTAAGAGATGACATTA	828
Qy	844	ACAGTATTAAGTCTCGCAATTAATTAATTTCCAAACTATGATCCACGATAGGATATCCATTAACA	903
Db	829	CTGGTATTAAGATTTGGTGGCGTTAATTTCCAAACTATGACACACATATGTATCCAAATCGAA	888
Qy	904	GTAATAAAACGAAATGACTAGGAAGTTTATACAGATCCAGTATAGGGTTTATCTGGGGTATTA	963
Db	889	ACAACAGCTCAACTTAACGGGAGTGTATACAGATCCGATAGCATTTTAACATAGTGACA	948
Qy	964	GAAGTGGAGGTAGCACTTACCTTGGTATATCTTAATTAATPACAACTTTACTGCTATG	1023

Db	949	AGTACTGATTTCTGCA---ACCTTGGTCAACCCACAGTGGTATTTCTTTTATGAAGTT	1005
Qy	1024	GAAAAATTAACCCAGACGACGTCCTCTTATACCACTTGGCTTAATGCTATTTTGTATAT	1083
Db	1006	GAAAAACAAGTAATTCCTCCGCACACCTTGTGTATCTCAGCTCAGTGAATAATTAAT	1065
Qy	1084	ACAAGACTCTAGAGTAATATGT-----CTGATGTGAAATAATTTGGGAGGCGCAT	1134
Db	1066	ACAAGTGAAGGGGTATTAAGTTAAATATGATGCAATATTAACATCTGTCAGAGCAT	1125
Qy	1135	ACATTACTTGAATAATGAAATGATGTTCTGAAATAAACCATTAACCTTGTGTAACCTGAT	1194
Db	1126	ACCTTAATAATATGCTGAACACGCTGATTCGACCGTAACATACACGCTAATTAACGGTCGA	1185
Qy	1195	TCTATTACTCTTATTCAAATTTTAAATTTTGGCAACCTTCTGTTTCAAGTATTTAGTCA	1254
Db	1186	ATCATCTTCAGAAAAAGAAATTCATTATTCGACCTTGAGATGAGGATTTTGTGAATTAATTC	1245
Qy	1255	CTTGCCTGTATATATTTAATGAGGAAACAGAGGCTTAATATATATTAAGTACAGTATAGA	1314
Db	1246	ACTGTGGCA---ACCTAGCTAAATTACTACCAAAAGGCATATGTGTGCCGGATCTTGG	1302
Qy	1315	GTCCTGAGAGTTATTTTAAATATATCATCAATATTAATTAATGATCCTGGATCTTTAAGATAC	1374
Db	1303	TTTCATATGTGTAAAAAAGGGAACTCATCAACAACAGCGTATTTATATTCAAAAACAT	1362
Qy	1375	GAAATGCTCTGTAATCTTCCATCCCAACATATATATCAGAAATTAACAGAGAAAGATTAAG	1434
Db	1363	ACAGCTCTCCAAAGGGGTACACAGGTTTAAAGATCAAGTATGAATAAATCCTTAAGATAGA	1422
Qy	1435	CCAAGACCAAAACGAGAGATTTCAAGCATATGATTTATCTAATATATCAAAATTTTGATGCA	1494
Db	1423	ACTGTACCGGTAGCTGAAGCTATATGCAATAGATTAATCTATATTAATCTCCCATTTCTTC	1482
Qy	1495	CGGCGAAGTATTCAGCGCGTATTTGTAATCTTTTAAAGTTTGATGGGACATACCAAGT	1554
Db	1483	TCTAAAAATGGAGGTGATATCTATGGGAGTTTCCGTGTAATTTGTTTGGACACATACAGT	1542
Qy	1555	ATGATATGTAATAATGCTCTTGAACAGATAAATTAATCTCAAAATAGATGCAAGTTAAAGGT	1614
Db	1543	GCGGATTTAAATATATCAATATATTTCAAGATMAAATCACTCAAAATTCACGCGGTAAAGGA	1602
Qy	1615	TGGGGGGGGAATATCGGGTTTGTATCCCAAGCATATGCG	1655
Db	1603	GACATGTTATATCTAGGGGCTTCGTAATGACAGGCTCCTGG	1643

RESULT 2
 US-07-812-180A-1
 Sequence 1, Application US/07812180A
 Patent No. 5366892
 GENERAL INFORMATION:
 APPLICANT: Foncecrada, Luis R
 APPLICANT: Payne, Jewel M
 APPLICANT: Sick, August J
 TITLE OF INVENTION: No. 5366892e1 Coleopteran-Active Bacillus
 TITLE OF INVENTION: Churingiensis Isolate and a No. 5366892e1 Gene Encoding a
 TITLE OF INVENTION: Coleopteran-Active Toxin
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Roman Saliwanchik
 STREET: 2421 N.W. 41st Street, Ste A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/812.180A
FILING DATE: 19920102
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Salimanchik, Roman
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
CLONE: 50C
US-07-812-180A-1

Query Match 12.5%; Score 256.2; DB 2; Length 3471;

Best Local Similarity 50.5%; Pred. No. 9.5e-53; Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

13 AAAAAATGAATGAATGAATGTTGATGCTTACGAATCAACTTAATGTCTAAT 72
10 AATATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 66
73 TGTATTCAGAGTATCCAGCAAAAGATCCAAATGACTATGCAACAGCACTAT 132
67 GATTCATACAGATACCTTTTGCAGATGACCAACAGATCGTTACAAATATGAT 126
133 AAGGAATGCTAATATGATGATGATGATGATGATGATGATGATGATGATGAT 192
127 AAGGATATCTGAAATGCTGGG-----GGAGGAATCTGAAATTA 168
193 TCTAGCCCTGAAGCTGCTTAAGTATGAGATGCTGTTTAAAGGATATTAACAGT 252
169 TTGGGAATCCGAGAGCTTTATTAATGATCCAGATTCAGATGGAATTTGGCAT 228
253 GGGATATACCTTGAATTTAGGGGTCCTTTGGCAATCATCTTTGGAATTAAT 312
229 GGTGATATAGAGAGCTTTAGGGGTTCCATTTGCTAGTCAGATAGCTTCTAT 288
313 AGGCTAATAGCTATTTTATGGGAG-----GGCTGATCATTTTGAAGCAT 366
289 TTCAATGTTGCTCAATTTATGCGCTCAAGAGCTATATATGAGGAGAAATTA 348
367 CTGTTGAAGAGCTTATTAAGAAAGATATGATCAGGCTGTAAGAGAAATGCT 426
349 CGAGTGAAGAACTCGTTGATCAAAAATGAAAATATATGTAAGTAAAGCT 408
427 GAGCTAGAAAGTTACAGGAATTTATGACTATATCAAACTAGACGACAGCA 486
409 GAATTAAGAGGCTAGGAATTTGCTTTGATGATATATGACGATCCTTGAAG 468
487 GTTAAACAGATGATG---ACATCGAGGGCACTAGTAACGCAATGCAATTT 543
469 GAAATTCGCAATATGCAAGAACTGAAAGTGTGTTCTATCAATTAATAGCT 528
544 AACTTTTGAAGAAATATGCAAAATTCAGGAAGAAACTTTGAATTTTATG 603
529 CTTAACCTTTGTTAGTTCAATTTCTTTTGGCAATCCGACAGAAATTAAT 588
604 CCAATATATGCAAGAGCTGGAATTTGATTTAATTTAAGAGATGCTGATTA 663

589 GCATATATGCAAGAGCTGGAACCTTATATTTATTTAAGATGCTTCTATTTT 648
664 GAGACAGTGGCAATTAAGTATGATGAATTCGTATATTAATTAATCACTACA 723
649 GAGAAAGTGGGATTTTACACAGGTAATTTCTGATTTTATTAATGCAATG 708
724 CTGATTAAGAAATTAAGATCAATTTATTAACATTTATTAACAGGTTTAA 783
709 CTTAACCGCTGAATTTGACATATTTGTAAGGATTAATAATCGCTTAAAT 768
784 AATGCTCAATGCTCAAGATTTGGTGAAGCTTTAATAGTTTGTATCAAGAT 843
769 AAGGTACCACTCTTAAGATTTGCTGAATTAATCATAGTTCTGTAAGATCA 828
844 ACATATTAATGATCTCGAATATTAATTTCAAACTATGATCAAGTATGATTA 903
829 CTGATTAATTAATTTGGTGGCTTATTTCCAACTATACACATATATGATCA 888
904 GTAAAAACGAATTTAGTGAAGATTTATTAACAGATCCAGTATGAGTTTAC 963
889 ACAACAGCTCACTTACACGGAGTGTATACAGATCCGATGATTAATCATG 948
964 GAAAGTGAAGTATGACTTACCTTGGTATATCTTAATTAATCACTTACGTA 1023
949 AGTACTGGAATTCGCA---ACCTTGGTCAACCAAGTGTATCTTTTATGA 1005
1024 GAAATTAACGAAGACAGCTCTTCTTATACCACTTGGCTTATGCTATTTT 1083
1006 GAAATTAACGAATTTGCTCGCCACACTTGTGATATATCTAGCTAGTAAT 1065
1084 ACAAGACTAGTAATATGT-----CTGATGGAATTAATTTGGGAGGCA 1134
1066 ACAAGTGAAGGGATTTATGATTAATATGATGATATTAATTAATCTAGT 1125
1135 ACATTAATGAATGAATGATGCTTCTGAATTAACCAATTAATTTGTTAA 1194
1126 ACCCTAATATGCTGAAGACAGCTGATTCAGCGTATCAACAGCTAATTA 1185
1195 TCTATTAATCTCTTATTAATTTTAAATTTGCGCACTTTCTGTTTCA 1254
1186 ATCACTTCAAGAAAGATTAATTTGATGATGATGATGATGATGATGAT 1245
1255 CTGCTGATTAATTTATTAAGGAGAACAGGCTAATTAATTAATTAATTA 1314
1246 ACTGTGCA---ACCTAGCTAATTAATTAACAAAGCATATGATGCGGAT 1302
1315 GTCTCGAGATTAATTTTAAATTAATCAATTAATTAATTAATTAATTA 1374
1303 TTCCATATGTTAAAGGGGAACTCATCAACAGCGTATTAATTAATTA 1362
1375 GAGTGTCTGCTATCTTCCATCCCAACTATTAATTAATTAATTAATTA 1434
1363 ACAGCTCTCCAAAGGTATTAACAGGTTTATGAATCAATGATTAATTA 1422
1435 CCAAGCAAAACCGAGAGATTTCAAGCATATTAATTAATTAATTAATTA 1494
1423 ACTGTACCGTACTGAAAGCTATATGATATGATTAATTAATTAATTA 1482
1495 CGGCGAAGTATTAAGCGGATTTGATCTTTTAAAGTTTGGTGGCAATCA 1554
1483 TCTTAATAATGAGAGTCACTATGAGGATTTCCCTGATTTTGGGACAT 1542
1555 ATGATGCTATTAATTAATGCTCTTGAACCAATTAATTAATTAATTAAT 1614
1543 GCGAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1602
1615 TGGGAGGAGAAATATCGGTTTGTATCCAGACTACTAGT 1655
1603 GACATGTTATATCTAGGGGTTCCGTAATGATCAAGGTCCTGG 1643

RESULT 3
US-08-315-468-1

Db	127	AAAGATTATCTGAAAATGCTGGG-----GGAGGAATCCCGAATTA	158
Oy	129	TCTAGCCCTGAAGGTGCTTAAAGTGTAAGATGCTGTTTAAACGGGATTTAAACAGTGA	252
Db	169	TTTGGAATCCGGAGACGTTTATTAGTTCAATCCAGATTCMAACTGGAATTTGGCATTTGTT	228
Oy	253	GGACATACTTTCGAAATTTAGGGGCTCTTTGGCAAGTCMAATCTTTGGAAATTAATAGT	312
Db	229	GGTGGAATATAGAGAGCTTTAGGGGTTCCATTTGGTCTAGTAGAGTAGTTCTAATAGT	288
Oy	313	AGGCTAATAGTATTTTATGGGCAG-----GGCTGATCCATTGGAAGCATTAATGCTT	366
Db	289	TTCAATTTGCTCAATTAATGCGCGTCAAGAGGCTAATATATGGGGAGAAATTAATGAA	348
Oy	367	CTTGTGAAGGCTTATTAAGAAAGATATGATCAGCGTGTAAGAGAAATGCTCTAGA	426
Db	349	CGAGTGAAGAATCCGTTGATCAAAAATATGAAAATATATGTAAGATTAAGGCTCTTGCT	408
Oy	427	GAGCTAAGAGGTTTACAGGAATTTAGATGACTATATCAAACTAGACTCAAGCATGCTGA	486
Db	409	GAATTTAAAGGCGTAGGAATGCTTTGAGATGATATAGCAGATCATTGGAAGATTTGGCTG	468
Oy	487	GTTAAACAAGATGATG--ACAATCGAGGGCAGCTAGTAAACGATATGCAATTTGTTGAT	543
Db	469	GAATATCGAATGATGCAAGAACTAGAAAGTGTTGTTCTAATCAATTTAATAGCTTTAGAT	528
Oy	544	AACTTTTCCAAAAGATATGCCAAATTCAGAGAAAGAAACTTGAATTTTATTTGTTA	603
Db	529	CTTAACTTTGTTAATCAATTCATCTTTTGGAGTATCCGAGACAGAAATCTATATTTA	588
Oy	604	CCAGTATATGCAACAGCCGGAATTTGCATTTAATTTAATTAAGAGATGCTGATTAATTT	663
Db	589	GCATTAATATGACAGCGCTGGAACCTACATTTATTTATTAAGAGATGCTCATTTT	648
Oy	664	GGACCAAGTGGCAATTAGTGATGATGAATTCGTGATTAATTAATCAACTACAAAGA	723
Db	649	GGAGAAGAGTGGGATTTTACACGAGGAATTTCTGATTTTAAATTCGCAAGTCAAA	708
Oy	724	CTGATTAGAAATTAAGATTCATTTGATTAACATCTTATAACAAGGATTTAAATCAATTT	783
Db	709	CTTACCGCTGAATTTGACATAATTTGTTAAAGTGATTAATAATCGGCTTAGATTAATTG	768
Oy	784	AATGCTCAATATGCTCAAGATTTGGGTAGGCTTTAATAGTTTCTGACAGATATGACATTA	843
Db	769	AAAGTACCACTTTTAAAGTTGGCTGATTAATCATCAGTTCCGTAGAGAGATGACATTA	828
Oy	844	ACAGTATTTAGATCTCGCAATATTTTCCAAACTATGATCCAGTAGATTCATTAAGA	903
Db	829	CTGGATTAATGATTTGGTGGCGTTATTTCCAAACTATGACACACATATGATTCCAATGAA	888
Oy	904	GTAATAACGAATTGACTAGGGAATTTATACAGATCCAGTAGGTTTACTGGGGTATTA	963
Db	889	ACAAACAGCTCAACTTACACGGGAGTGTATACATCCAGATGATTTTAACATATGACAA	948
Oy	964	GAAGTGGAGGTAGGACTTACCTTGGTATATCTTATAATAACAACCTTTACTGCTATG	1023
Db	949	AGTACTGATTTCTCA--ACCCTTGGTCAACCAAGTGTATTTCTTTTATGAAGTT	1005
Oy	1024	GAATAATACGACAGACGACGTCTTTCTTATACACTTGGCTTAATCGTATTTTGTATAT	1083
Db	1006	GAATAACAACGTAAATTCGTCCGCGCACACTGTTTGTATTAATCTCAGCTCAGTAGAATAAT	1065
Oy	1084	ACAAAGACTTAGTAAATATGT-----CTGATGTGAAATATTTTGGGAGGGCAT	1134
Db	1066	ACAAATGAGGGGATTTACCTTAATATATGATCCATATATAACTACTGGTCCGAGACAT	1125
Oy	1135	ACATTAATGTTGAATATGAAATGATGTTTGGAAATTAACCCATACTTTGGTAAACATGAT	1194
Db	1126	ACCCTAATATATCGTAAGACGCTGATTTCCACGTTACATACACAGCTAATTAACGCTGA	1185
Oy	1195	TCATATTAATCCATATCAATATTTAATTTTGGCAACCTTTCTGTTTTCAGTATTAAGTCA	1254
Db	1186	ATCACTTCAGAAAAGAAATTAATTTGCACTTGAGATATGGGATATTTTGAATTAATCA	1245

QY 1255 CTGCTGTAATATTTAGAGAGAAAGGCTTAATATTAATTAAGTATGCAATGATGA 1314
 DB 1246 ACTGTGGCAA---ACCTAGCTAATTAATCAACAAAGGCAATATGTCGCCGATCTTGG 1302
 QY 1315 GTCTCGAGATTAATTTTAAATACATCAAAATATAATATGATCTGATCTTTAAGATAC 1374
 DB 1303 TTCATATGTTAAAGGAGGAACTCAACAAACAGCTATTTATTAATCAAAAACACAT 1362
 QY 1375 GAAGTCTGCTAATCTTCCATCCCAACATATATTAATCAAGATTAACAGAAAGATAG 1434
 DB 1363 ACAGCTCTCAAGGGGTACACAGTTTATGAATCAAGTATGAAATATCTTAGATAGA 1422
 QY 1435 CCAAGACCAAGAGAGAGATTTTCAGCCATAGATTAATTAATCAAAATTTTGATGCA 1494
 DB 1423 ACTGTACCGTAGCTGAAGCTATATGATATATTAATTAATTAATCTCCATCTTTC 1482
 QY 1495 CGCGAGATTAATCAAGCGATATTTAGTCTTTTAAAGTTTGGTGGCAATACCAAGT 1554
 DB 1483 TCTAAATAGGAGTGATATGATAGGAGTTTCCCTGATTTTGGACACATTAAGT 1542
 QY 1555 ATGATCTGTAATATCTCTTGAACGATTAATTAATTAATTAATGATGCAATTAAGT 1614
 DB 1543 GCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1602
 QY 1615 TGGGGGGGGAATATCGGCTTTGTCATCCCAAGACCTACTGG 1655
 DB 1603 GACATTTATATCTAGGGGGTCCGTAATAGAGGGTCTGG 1643

RESULT 4

US-07-941-650A-1
 Sequence 1, Application US/07941650A
 Patent No. 6294184
 GENERAL INFORMATION:
 APPLICANT: Uyeda, Kendrick A.
 APPLICANT: Bradfisch, Gregory A.
 TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/941.650A
 FILING DATE: 19920308
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/758,020
 FILING DATE: 12-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/658,935
 FILING DATE: 21-FEB-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/642,112
 FILING DATE: 16-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3471 base pairs

TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: kumamotoensis
 INDIVIDUAL ISOLATE: P850C
 IMMEDIATE SOURCE:
 CLONE: E. coli NM522 (pMYC1638), NRRL B-18751
 US-07-941-650A-1

Query Match 12.5% Score 256.2; DB 3; Length 3471;
 Best Local Similarity 50.5%; Pred. No. 9.5e-53;
 Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;
 QY 13 AAAATATAAATGAAATATGATGATGCTTTAAGATCAATCTTAATATGCTAAT 72
 DB 10 AATATCAAAATGAAATATGAAATTTATAGATGCAACCTTCTAATC---TGATCCAGT 66
 QY 73 TGTATCAAGATATCACTAGCAAAAGATCCCAATGACTATGCGAAACAGACTAT 132
 DB 67 GATTTAACAAGATACCTTTTGGCAATGAGCCAAAGATGCGTTACAAATATGAATAT 126
 QY 133 AAGAAATGCTAATATGATGATGATGCAATATTAATGATATTAAGACAGTAT 192
 DB 127 AAGAAATATCTGAATATGCTGGG-----GAGGAATCTGAAATTA 168
 QY 193 TCTAGCCCTGAAGCTGCTTAATGATGATGATGCTGTTTAAAGGATATTAACAGTGA 252
 DB 169 TTGGAAATCCGAGAGCTTATTAATGATCAACAGATTAATGCAATGCAATTTGCAATGTT 228
 QY 253 GGAATATCTTCAATTTAGAGGCTCTTGGCAAGTCAATCAATTTGAATATTAAT 312
 DB 229 GGTGCAATCTAGAGACTTTAGGGGCTTCCATTTGCTAGTCAAGATGATCTTCTAAT 288
 QY 313 AGCTAATGATATTTATAGGGGAG-----GGCTGATCATTTGAGCACTTAATGTT 366
 DB 289 TTCAATGTTGCTAATTAATGAGCCGCTCAAGAGGATGATATGAGGAGAAATTAAGAA 348
 QY 367 CTGTTGAAGAGCTTATTAAGAAAGATATGATCAAGCTGTAAGAGAAATGCTTTAGA 426
 DB 349 CGATGGAAGAACTCGTTGATCAAAAATGAAATATGTAAGATTAAGGCTCTTGGT 408
 QY 427 GAGCTAAGGTTTACAGGAAATTAATGATGATATCAAACTGACTGACAGATGCTA 486
 DB 409 GAATTAAGAGGCTAGGAAATGCTTGGATGATATGACAGATCACTTGAAGATGGCTG 468
 QY 487 GTTAACAAGATGATG---ACATGCGAGGCACTAGTAACGAGATATGCAATTTGAT 543
 DB 469 GAAATGCAATATGCAAGAACTGAAAGTGTGTTCTAATCAATTTATAGCTTAAGAT 528
 QY 544 AACTTTTGAAGAATATGCCAAATTCAGAAAGAAACTTTGAAATTTTATTTGTTA 603
 DB 529 CTTAATCTTTGATGCTCAATTCATCTTTTGGAGATCCGGAAGACAGATATTAATTA 588
 QY 604 CCAATATGACAGAGCCGGAATTTGATTAATTTATTAAGATGCTGATTAATTTT 663
 DB 589 GCAATATGACAGAGCTGGAACCTAATTTATTTATTAAGATGCTGCTTAATTTT 648
 QY 664 GAGCAGATGCGAATTAAGTATGATGAAATTCGATATTAATTAATGAGACTACAAGGA 723
 DB 649 GAGAAAGAGTGGGAATTTACCAAGGTGAATTTCTAGATTTATTAATGCTCAAGTCAA 708
 QY 724 CTGATTAAGAAATATTAAGATCAATTTATTAATCAATTTATTAATGATTAATTT 783
 DB 709 CTACCGCTGAATATCAAGCTATTTGATTAATGATTAATTTGCTTAATTAATTTG 768
 QY 784 AATGCTCAATGCTCAAGATTTGGTGAAGCTTTAATGATTTGTAACAGATATGACATTA 843
 DB 769 AAGGATACCACTTCAAAAGTTGGCTGAATTTATCAATCAATGCTGAGAGATGACATTA 828

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QY      844 ACAGATTAGATCTCGCAATATTATTTCCAACTATGATCCAGTAGTATTCATTAGCA 903
      829 CTGGTATTAGATTGGTGGCGTTATTTCCAACTATGACACATATGATTCACATCGAA 888
QY      904 GTTAAAAACGGAATTGACTAGGGAAGTTTATACAGATTCAGTAGGTTTACTGGGGTATTA 963
      889 ACAACAGCTCACTTACACGCGGATGTGTATACAGATCCGATACCATTTTAAATAGTAC 948
QY      964 GAAAGTGAAGTGAAGCTTACCCCTGGTATATCTTAAATATCAACCTTACTGCTATG 1023
      949 AGTACTGGATTTGCA---ACCCTTGGTCAACCCACAGTGTATCTTTTATGAAGTT 1005
QY      1024 GAAATATACGCAAGACGAGCTCTTCTTATACCACTGGTTAATGTAATTTTGTATAT 1083
      1006 GAAACAGCTAATTCGTCGCCACACTGTTGATATACTACGCTCAGTAGAAATTAAT 1065
QY      1084 ACAAGACTTAGTATATGT-----CTGATGTGAAATATTTGGGAGGGCAT 1134
      1066 ACAAGTAGAGGGGTATTTACGTTAAATATATGATGATATATTAACCTACTGCTCAGACAT 1125
QY      1135 ACATTAAGTAAATGGAATATGATGTTCTGAATAATACCATTAACCTTTGGTAAACGTAT 1194
      1126 ACCCTAAATATATGTAGAACAGCTGATTTGCAACCTATACATACAGCTAATTCAGGTCCA 1185
QY      1195 TCTATTACTCTTATTCATATATTTTAAATTTTGGCAACCTTTCTGTTTCAATATGAGTCA 1254
      1186 ATCACTTCAAGAAATATCATTTGCACTTGAGGATGAGGATATTTTGAATTTAATTTCA 1245
QY      1255 CTGCTCTGATATATTTAGAGGAAACAGAGGCTATATATATTTACTAGTACTGATGTA 1314
      1246 ACTGTGGCAA---ACCTAGCTAATTTACTACCAAAAGGCAATGTGTGCGGAGTCTTGG 1302
QY      1315 GTCTCGAGAGTATTTTAAATATATCATCAATATATATATGATCTTAAAGTATC 1374
      1303 TTTCATATGTTAAAAAGGGAACCTCTCAACAGACCGATTTATATTTAAAAACAT 1362
QY      1375 GAAGTCCGTCTATCTTCATCCCAACATATATTTATCAGAAATTTACAGAAAGATAG 1434
      1363 ACAGCTCTCAAGGGGTATACAGAGTTTATGATATCAAGATGATAATTAACCTAGATAGA 1422
QY      1435 CCAGACCAACGCAAGAGATTTACGCAATGATATCTTATATATCAATTTTGATGCA 1494
      1423 ACTGTACCGGTACTGAACCTATAGCATATATCTCATATTAATCTCCATCTTTTC 1482
QY      1495 CGGCGAAGTATGTTACGCGGTATTTGATGCTTTTAAAGTTTGGTGGGCAATACAGT 1554
      1483 TCTAAAAATGGAGTCACTATGGAAGTTTCCCTGATTTTGTGGACACATACTAGT 1542
QY      1555 ATGATCGTATATATGCTTGTGAACCATTAATTAATTAATTAATGATGCAATTAAGT 1614
      1543 GCGGATTTAAATATATCAATATATTTGATGATTAATCACTCAATATCCAGGGTAAAGGA 1602
QY      1615 TGGGGGGGGAATTCGGGTTTGTATCCCAAGACACTACTGG 1655
      1603 GACATGTATATCTAGGGGTTCCGTATGACAGGGTCTTGG 1643

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RESULT 5
US-10-089-678-2
; Sequence 2, Application US/10089678
; Patent No. 6962977
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shunichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02

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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(3501)
; OTHER INFORMATION:
US-10-089-678-2

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Query Match      11.5%; Score 236; DB 3; Length 3504;
Best Local Similarity 55.9%; Pred. No. 8.3e-48;
Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

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QY      13 AAAAAATGAATGAATGAATGTTGATGGCTTTGAGATCAACTTAATATGCTAAT 72
      10 AATATCAAAATGAATGAATGAATTTAGATGCTTCACTA---CTTCTGATTCGAT 66
QY      73 TGTATCAAGGATATCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
      67 AATTCTTATGATACCTTTAGCAAAAGATCAAGACCAATTAACAAACATGAACCTAT 126
QY      133 AAGAAATGCTAATATGTGTGATTCAAATACAAATTTATGTTGATATTAAGACGTAT 192
      127 AAGATATATCTGAGATGCTGAG-----GGAGAGATCTGAAATTA 168
QY      193 TCTAGCCCTGAAGCTCTTTAATGATGAGAGATGCTGTTTAAACGGGTATTAACAGTGA 252
      169 TTGGAATCCGAGACGTTTATTTAGTCACTACGTTCAAACTGAAATTTGCAATTTG 228
QY      253 GGGCATATCTTTCGAATTTAAGGGGCTCTTGGCAAGTCAATCATTTGGAATTAATGAT 312
      229 GGTCAAGTACTGGGGGCTTTAAGGGGTTCCATTTGCTGACAGATACCTAGTTTATATG 288
QY      313 AGGCTATATGATTTTATATGCGGAGGCGCT-----GATCATTGAAGACCTTAATGTT 356
      289 TTCAATTTGCTCAATTTATATGCGCATCAAGTACCGTATGATGATGGAATATGATTAAGAA 348
QY      367 CTGTTGAAGAGCTTATTAAGAAAGTATATGATCAGCTGTATAGAGAAATGCTCTTGA 426
      349 CAATGGAAGATCTAATTAATTAATCAAAATTAACAGATTTCTGTATAGAAACAGCGCTTGA 408
QY      427 GAGCTAAGAGTTTACAGGAAATTTATGACTATATCAATCACTAGCTGACAGAGCTTA 486
      409 GGCATACAAAGATTTAGGATGGCTTAGACGATATACAGAAATCACTTAAGAAATGGCTG 468
QY      487 GTTACAGAAATGATGACA---ATCGAGAGGCACTATGTAACGATATGCAATTTGAT 543
      469 GAAATCGTATATGATTCAGAGCTGAAAGTGTGTGTGTAACCCAAATATATAGCTTTAAG 528
QY      544 AACTTTTGAAGAAGATATGCGCAAAATCAAGAAAGAACTTTGAATTTATTTGTTA 603
      529 CTGATTTTGTGCTAATAATCCATCTTTTGAATATCTGACAGAGATACATTAATTA 588
QY      604 CCAGTATATGACAAGACCGCAATTTGCAATTTATTTATTAAGATGCTGATTAATTT 663
      589 TCAGTATGACACAGACAGAAATTTACATTTGCTATTTATGAGATGCTTCATTTT 648
QY      664 GGAGCAGCTGGCAATTAGGTGATGAAATTCGTATTAATTTATTCAGACTCAAGGA 723
      649 GGAGCAGAGTGGGGAATTCACACAGAGAAATTTCCACATTTTATGATGTCAGGTGACA 708
QY      724 CTGATTAAGAAATATTAAGATGATTTATATCACTTATACCAAGGTTTAATCAATTT 783
      709 CGTACCGCCCAATCTCGGATTTATGTGTAAAGTGTATTAACCTGCTTAGTAAATTTA 768
QY      784 AATCGTCAATATGCTCAAGATTTGGTGAAGCTTTAATAGGTTTGTGTCAGATATGACATTA 843
      769 AAGATGCAATGCTGCAAGTGTGCTGAGATACCAATTCGAGAGAAATGACATTTA 828
QY      844 ACAGATTAGATCTCGCAATATTTATTTCCAACTATGATCCAGTAGTATTCATTAGCA 903

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Accession	Sequence	Position
Db	CTGGTATTAGATTTAGTAGCGTTATTCCAACTATGACACAGTACGTATCCATCGAA	888
Qy	GTAAAAACGGAATTGACTTGGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTATTA	963
Db	ACAAAGGCCCACTTACACGGGAAAGTATACAGATCCAAATGATTATTAACAGAGAAACA	948
Qy	GAAGTGGAGTAGGA	979
Db	AGTGATGATTTTGT	964

RESULT 6
 US-10-089-678-3
 Sequence 3, Application US/10089678
 Patent No. 6962977
 GENERAL INFORMATION:
 APPLICANT: ASAHO, Shinichi
 TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
 TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
 FILE REFERENCE: Q68821
 CURRENT APPLICATION NUMBER: US/10/089,678
 CURRENT FILING DATE: 2002-04-03
 PRIOR APPLICATION NUMBER: JP 2000-236140
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: PCT/JP01/06660
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 3690
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 US-10-089-678-3

Query Match	11.5%	Score 236	DB 3;	Length 3690;
Best Local Similarity	55.9%;	Pred. NO. 8.4e-48;		
Matches 546;	Conservative	0;	Mismatches 400;	Indels 30;
				Gaps 4

Qy	13	AAAAATAAAATGAATATCAAAATGTTGATGTCTTACGATCAACTATATATGTCTAAT	72
Db	196	AATATCAAAAATGAATATGAATTTCTAGATGTCTTATCATCTA---CTTCTGATTCGAT	252
Qy	73	TGTTATCCAGGTATCCACTAGCAAAAAGTCCAAATATGCTATGCGAAAACGAACTAT	132
Db	253	AATTCGTAGATACCTTCTTACCAACGATCAACGACACATTTACAAAACATGAACCTAT	312
Qy	133	AAAGAAATGGCTAAATATGTGTGATTTCAATATACAACTTATTTGTGTATTAAGACGTAT	192
Db	313	AAAGATTTATCTGAGAAATGCTGAG-----GGAAAGAACTCTGAATTA	354
Qy	193	TCATACCCCGAAGCTGCTTTAAGTGAAGAGATGCTGTTTTAACGGGTATTAACAGTGA	252
Db	355	TTTGGAATATCCGAGACGTTTATTTAGTCACTTACGTTTCAAATCGAATTTGCATTTGT	414
Qy	253	GGGACTATATCTTCGAATTTAAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAATAGT	312
Db	415	GGTCAAGTACTGGGGGCTTTAGGGGTTTCATTTGCTGGAACAGTACTAGTTTATADGT	474
Qy	313	AGGCTAATAGTATTTTATATGGGACGGGCT-----GATCATTTGAAGACCTTATAGTT	366
Db	475	TTCATTTGTCGGTCAATTATGGCCATCACTACAGTACGTAAGTATGGGAAATGATTTATGA	534
Qy	367	CTTGTTGAAGAGCTTATTAAGAAAAGTATAGATCAGCGTGAAGAGAAAATGCTCTTAG	426
Db	535	CAGGTGAAGAGCTTATATGATCAAAAATAACAGATCTTGTAAGGAAAACAGGCGTTTGA	594
Qy	427	GAGCTAGAAAGTTTACAGGGAATTAAGAACTATATCAACTGACCTGCAGACATGGCTTA	486
Db	595	GGACTACAAGGATTTAGGAGATGGCTTAGACGATATATCAGAAATCACTTAAGAATTTGGCTG	654
Qy	487	GTTAACAAAGATGATGACA---ATCGAGAGGCACTAGTAAACGAGTATGCAATTTGTTGAT	543

Db	655	GAAATTCGTATGATATACAAAGAGCTAGAAAGTGTGTGGTACCCCAATATATAGCTTTGAG	714
Qy	544	AACTTTTTCGAAAAGAAATATGCCAAAATATCAGAGAAAGAAACTTTGAAATTTTATTCGTA	603
Db	715	CTGATATTTTGTCTTAATAATCCATCTTTTGGCAATATCTGGACAGAGATGCCATATTA	774
Qy	604	CCAGTATATATGCACAAGCCGCGCAATTTGCATTTAATTTTATTTAAGAGATGCTGATTAATTTT	663
Db	775	TCAGTGTATGTACAAAGCAGGCGAATTTACATTTGTGTATTTATAGAGATGCTCCATTTT	834
Qy	664	GGAGCACATGTGGCAATTATGTTAGTATGAAATTTGCTGATATTTATTCACACTACAAAGA	723
Db	835	GGACACAGTGGGGATTTCAACAGAGAAATTTCCATTTTATGATTCGTCAGGTGACA	894
Qy	724	CTGATTTAGAGATTTTAAAGATCATTTGATATACTTTATATAACGAGGTTTAAATCAATTT	783
Db	895	CGTACCCGCCAATACTCGGATTAATTTGTGTAAAGTGATATAACATGGCTTATGATTAATTA	954
Qy	784	AATGCTCAAAATGCTCAAGATTGGGTAGCTTTAATATAGTTTCTTACAGATATACATTTA	843
Db	955	AAAGGTACGAATGCTGCMAAGTTGGCTGAAGTATCACCAATTTCCAMAGAAATATACATTTA	1014
Qy	844	ACAGTATTTAGATCTCGCAATTTATTTTCCAAACATATGATCCACGTAGTATTCATTTGCA	903
Db	1015	CTGGTATTTAGTTTATAGTAGCGTTATTTTCCAAACTATATACACAGTACGTATCCATCGAA	1074
Qy	904	GTTAAAAACGAATTGACTTATGAGGAAGTTTATACAGATCCAGTAGGAGTTTACTGGGGTATTA	963
Db	1075	ACAACGGCCCAACTTACACGGGAAGTGTATACAGATCCATATGATTTTAAACAGAAACA	1134
Qy	964	GAAATGAGAGTACGA 979	
Db	1135	AGTGTGATTTGTATA 1150	

RESULT 7
 US-08-315-468-3
 ; Sequence 3, Application US/08315468
 ; Patent No. 5554534
 ; GENERAL INFORMATION:
 ; APPLICANT: Michaels, Tracy Ellis
 ; APPLICANT: Fonseca, Luis
 ; APPLICANT: Narva, Kenneth E.
 ; TITLE OF INVENTION: Process for Controlling Scarab Pests
 ; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/315,468
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/014,941
 ; FILING DATE: 01 FEB 1993
 ; APPLICATION NUMBER: 07/828,430
 ; FILING DATE: 30-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/808,316
 ; FILING DATE: 16-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Bacillus thuringiensis*
STRAIN: kumamocensis
INDIVIDUAL ISOLATE: 50C
IMMEDIATE SOURCE:
LIBRARY: LambdaGEM-11(crm) library of L. Foncerrada
CLONE: 50C(b)
US-08-315-468-3

Query Match 11.5%; Score 235.6; DB 2; Length 3507;
Best Local Similarity 56.5%; Pred. No. 1e-47;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAAATGAATGATGAATGTTGATGCTTTACGATCACTCTATATGCTAAAT 72
DB 10 AATTAATCAAAATGAAATGAAATTTATAGATGCGACACCTTCTATCCTC---TGATCCAAAT 66
QY 73 TGTATCCAGATGATCCACTAGCAAAAAGATCCCAAAATGACTATGCGAAACAGAACTAT 132
DB 67 GATTCACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTACAAATATGATATAT 126
QY 133 AAGAAATGGTAATATGATGATGATCAATATGATGATGATGATGATGATGATGAT 192
DB 127 AAGATATTTTAAATATGCTGCGGAA-----TGATGATATACCT 171
QY 193 TCTAGCCCTGAAGCTCTTTAAGTATGATGATGATGATGATGATGATGATGATGAT 252
DB 172 GGTTCACCTGAGATATTTCTAAGCGAAGATGATGATGATGATGATGATGATGATGAT 231
QY 253 GGGACTATATCTTGAATTTAGGGGTCCTTTGGCAATGATCAATTTGGAATTAATAGT 312
DB 232 GGTAAATTAATAAGATTTAGGGGTCCTTTGTTGGGCGATGATGATGATGATGATGAT 291
QY 313 AGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
DB 292 CAATTAATGATATCTGTCGCTTCAAAACAAAGATCAATGGAATTTTATGAA 351
QY 367 CTGTGTAAGAGCTTATTAAGAAAGATATGATGATGATGATGATGATGATGATGATGAT 426
DB 352 CAAGTGAAGATATCTATTAATCAAAATATGCAAGATATGCAAGATATGCAAGATATGCA 411
QY 427 GAGCTGAAGGTTTACAGGAATTTAGAGATTAATCAAACTAGACTGCAAGATGCTA 486
DB 412 GAATGGAAGGCTAGGATATTAATCAATTAATCAATCAATCAATCAATCAATCAATCAAT 471
QY 487 GTTAACAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
DB 472 GAAATCCCAATGTTCAAGAGCTTACGATGATGATGATGATGATGATGATGATGATGAT 531
QY 544 AACTTTTGAAGAAATATGCCAAATTTCAAGAAAGAAACTTTGAATTTATTTGTTA 603
DB 532 AGTTTATTAACGAATATATGCAATCTTTGAGTGAAGAAATTTGAGTGAATTTGCTT 591
QY 604 CAGTATATGACAAAGCCGGAATTTGATTTAATTTATTAAGATGCTGATTTATTTT 663
DB 592 ACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
QY 664 GAGACACAGTGGCAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 723
DB 652 GGAGAAAGATGGGATTTCTTACAGACATTAATTAATTAATTAATTAATTAATTAATTAAT 711

QY 724 CTGATTTAGGAATATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
DB 712 CTACTGACGAATATTTCTGACCACTGATGAAGGTATGAAGAACTGTTAGCAAAATTA 771
QY 784 AATCGCTCAAAATGCTCAAGATTTGGGAGCTTTAATAGGTTTGTACAGATATGACATTA 843
DB 772 AAGGCTCGAGCGCTTAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 831
QY 844 ACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
DB 832 ACGGTGTTAGAGTGTGTTGATTTTCAAACTATGATACGGTATCGATATCCACTGGCA 891
QY 904 GTAAAAACGAAATTTGACTGAGGAAGTTTATTAACATCCAGTAGG 947
DB 892 ACAACAGCTCAGCTTAACAAGGAAGATATTAACAGATCCACTGG 935

RESULT 8

US-08-286-870A-5
Sequence 5, Application US/08286870A
Patent No. 6063605

GENERAL INFORMATION:

APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TIPPERT, JM
APPLICANT: BLENN, RG
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DABRY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,870A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435

Prior Application Data:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990

Prior Application Data:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: PAUL N. KOKULIS

REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000
TELEFAX: (202) 823-0944
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 1..1607

US-08-286-870A-5

Query Match

11.3%; Score 231; DB 3; Length 1607;

Best Local Similarity 51.2%; Pred. No. 1,1e-46;
Matches 714; Conservative 0; Mismatches 645; Indels 36; Gaps 6;

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Qy 230 TTTTAAAGGTTATTAACAGTGTAGGAGCTATCTTGGAAATTAAGGGTCCCTTGGCAA 269
Db 179 TTTAAACAGGTATTTGATTTGCGGGTAAATTAATCTGTACCTTGGGCTTTTTCAG 238
Qy 290 GTCAATCATTTGGAAATTAATAGTGTAGTATTTTATGGGCA---GGGCTGATC 346
Db 239 GACAAAGTGTAGTCTTTATATGTTTATCTTAGTGAGCTATGCGCTTAAGGGAAAAATC 298
Qy 347 CATTTGAAGCACTTATGTTCTTGTGTAAGAGCTTATTAAGAAAGATTAAGATCAGGCTG 406
Db 299 AATGGGAATCTTTATGGAACATGTAGAAAGATTTATTAATCAAAAATATCAACTATG 358
Qy 407 TAAGAGAAATGCTCTTGAAGAGTAAAGGTTTACAGGAATTAAGAGTATATCAAA 466
Db 359 CAAGAAATTAAGCACTTAAGAGCTTGAAGAGATTAAGAGATGCTTATGCTTACCATG 418
Qy 467 CTAGACTGCAAGCATGCTGATTAACAAGATGATGACA---ATCGAAGGCACTAGTAA 523
Db 419 ATTGCTGTAAGATGTTGGTGTGAATGCTATTAACACAGGGCTAGAGTGTGTCAAGA 478
Qy 524 CGCAGTATGCAATGTTGATTAATCTTTGAAAAGAAATATGCCAAATTCAGAGAAAGAA 583
Db 479 GCCAATATATCGCATTAAGAAATGATGTTGCTTGAAGAACTACCTTTTTCAGAGTCTG 538
Qy 584 ACTTTGAATTTTATTTGTACCAATATATGCAACAGCCGGAATTTGCAATTTATTTAT 643
Db 539 GAGAGAGGTACCACTTAATTCAGATATATGCCCCAAGCTGCAAAATTAATCTTGTGTAT 598
Qy 644 TAAGAGATGCTGATTAATTTTGGAGCAAGTGGCAATTAAGGATGATGAATTCGTGATA 703
Db 599 TAAGAGATGCTGATTAATTTTGGAGCAAGTGGCAATTAATGATGATGATTTTCAACAT 658
Qy 704 ATTATATCAGACTTACCAAGAGCTGATTAAGAAATTAAGATCAATTTGATTAACATTTATA 763
Db 659 TTTATATACGTCAGATGGAAGAGAGAGATTAATTCGCAATGTTGTGAATGTGATATA 718
Qy 764 ACCAGGTTTAAATCAATTTAATGCTCAAAATGCTCAAGTTGGGTAGCTTAAATAGT 823
Db 719 GCACAGGTCTAAATTAACCTTAAGGGGTAAATGCGGAAGTGGGTACGATTAATATCAAT 778
Qy 824 TTGATCAGATATGACATTAACAGTATTAATGCTCGCAATTAATTTCCAACTAGATC 883
Db 779 TCCGTAGAGCAATGATCTTAATGCTAGATTAATGAGCACTTAATTTCCAACTAGATC 838
Qy 884 CACGTAGTATCATTAGCAGTAAAGAAAGGAAATTTAGTGAAGTATTAACAGATCAG 943
Db 839 CACAATATGATTCATTAATAAAGTCAAGCCCACTTAAGAGAAAGTATTAACAGAGCAA 898
Qy 944 TAGGTTTACTGAGGATTAAGAAAGTGAAGTGAAGCTTACCTTGTGATTAATCTTAATA 1003
Db 899 TTGGG---ACAGTACATCCCATCCCAAGTTTACAGTACAGACTGGTATTAATTAATATG 955
Qy 1004 ATACAACCTTATCTGCTATGAGAAATTAACCAAGAGAGAGCTCTTCTTAATCAACTGGC 1063
Db 956 CACCTTGTCTCTGCTATGAGAGGCTGCTGTGTTGCAAAACCGCATCTACTGCAATTTTC 1015
Qy 1064 TTAATGATATTTTGTATATA---CAAGACTAGGTAATATGCTGATGTGAGAAATA 1120
Db 1016 TAAGAAAGTATTAACATTTAGAGCTTATTAAGTGAAGTGAACACTCAATTAATGAATA 1075
Qy 1121 TTTGGGAGGAGCATCACTTAATGTAAGAAATGAATGATGTTCTGAATAATCACTTACT 1180
Db 1076 TGTGGGAGAGCAATTAATGTAATTCGAAACAATAGAGAGAAAGCTTAATTAATCAACAC 1135
Qy 1181 TTGGTAAACGATTTCAATTAATCTCTATTCATTAATTTTATTTTGGGAACCTTCTGTTT 1240
Db 1136 AAGGATTAATTAATTAATCTCTATTAATCTCTGTAACATTAACGTTTCTGAGAGCTCT 1195
Qy 1241 TCAGTATGAGTCACTTGTCTGATATATTAATTAAGAGAGAGAGGCTTAATTAATTAATA 1300

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Db 1196 ATAGAGCTGATCATTTGGCAGGGCTGAATCTATTTTAACTCAACCTGTTAATGAGTAC 1255
Qy 1301 CTAGTCAGTATGAGAGTCTCGAGAGTATTTTATTAATCATCAATTAATTAATGATGACTG 1360
Db 1256 CTAGGTTGATTTTCAATGGAATTTGTCACACATCGATCGATCTGATTAATTC----- 1311
Qy 1361 GATCTTTAAGATACGAAGTCTGCTAATCTTCATCCCAACTAATTAATTAATGAAATTAC 1420
Db 1312 --TATTATCAGAGGTATGCTGAATTTGGACGCAATTACAGATTCAGAAATGAATTAC 1369
Qy 1421 CAGAAAGATTAAGCCAAAGCAAGCAGAGAGATTTACGCAATTAATTAATTAAT 1480
Db 1370 CACCTGAGCAACAGACAGCCAAATTAACAAATTAATGATCAATTAATTAATCAATAG 1429
Qy 1481 CAATTTTATGACAGGCGAAGTATTCAGGCGGTATGTTAGTCTTTAAGCTTGGTT 1540
Db 1430 -----GACTCATTTCAACATCAATGAGAGAGAGATTTGATTTCTT 1471
Qy 1541 GGGCAGATACAGATATGATCGTAAATGCTTGAACCAATTAATTAATTAATTAAT 1600
Db 1472 GAGCGATGATGATGAGATGATGATCAAAATTAATTAATTAATTAATTAATTAAT 1531
Qy 1601 ATGCACTTAAGGTT 1615
Db 1532 CATTAAGTAAAGCTT 1546

RESULT 9
US-08-286-870A-3
; Sequence 3, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAYLOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLUNK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1946 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1946
 US-08-286-870A-3

Query Match 11.3%; Score 231; DB 3; Length 1946;
 Best Local Similarity 51.2%; Pred. No. 1.1e-46;
 Matches 714; Conservative 0; Mismatches 645; Indels 36; Gaps 6;

```

QY 230 TTTTAAAGGCTATTAACAGGTAGGAGCTATCTTGAATTTAGGGGCTCCCTTGGCAA 289
DB 179 TTTCAACAGGTATTTGGTATTTGGGCTAAATCTGTACCTTAGGGGCTCTTTTGGCAG 238
QY 290 GTCAATCATTTGGATTAATAGAGCTAATAGGATTTTATGGGCA---GGGCGTATC 346
DB 239 GACAACTAGCTAGCTTTTATATGTTTATCTTAGGTGAGCTAGTGGCTTAAGGGGAAAAATC 238
QY 347 CATTTAGAGCACTTATGCTTCTTGGTAGAGCTTATTAAGAAAAGTATAGATCAGGCTG 406
DB 299 AATGGGAAATCTTTATAGAAACATGTAAGAGATTTATATCAAAAAATATCAACTTATG 358
QY 407 TAAGAGAAATGCTCTTAGAGAGCTAGAGGTTTACAGGAATTTAGACTATATCAAA 466
DB 359 CAAAGAAATTAAGCACTTACAGACTTGAAGAGATTTAGAGATGCTTACCTTACCATG 418
QY 467 CTAGACTGCAAGAGTGGCTAGTTTAAAGAAATGATGCA---ATCGAGGGGCACTAGTAA 523
DB 419 ATTCCGTTGAAAGTTGGGTTGAAATCTATATACACAGAGGCTAGAGTGTGTCAAGA 478
QY 524 CGCAGTATGCAATTTGTTGATTAATCTTTTGGAAAAGATATGCCAAATTCAGAAAAA 583
DB 479 GCCAATATATCGATTAGATATGATGTTGCTTGGAAAATCACTTCTTTTGGAGTGTCTG 538
QY 584 ACTTTGAAATTTTATTTGTTTCCAGTATATGCAACAGCCGCAATTTGCATTTATTTTAT 643
DB 539 GAGAGGGGTACCATTTATTTCCGATATATCCCAAGCTGCAAAATTTTCAATTTCTGTAT 598
QY 644 TAAGAGTGTGATTTATTTTGGAGCACTAGTGGCAATTAAGTGAATGAATTCGATAT 703
DB 599 TAAGAGTGTGATTTATTTTGGAGCACTAGTGGCAATTTATATCTTCAAAAATTTCAACAT 658
QY 704 ATTATATCACTATCAAGAGCTATTAAGAGATTAAGATCAATTTGATTAATCACTTATAT 763
DB 659 TTTATATACGCTCAAGTCGAACGAGAGATTTATTCGACATTTGTGTGAATATGATAT 718
QY 764 ACCAGGTTTAAATCAATTTATTCGCTCAAAATGCTCAAGTTGGGTAGCTTTAATAGGT 823
DB 719 GCACAGGTCTAAATTAATCTTGAAGGGGTACAAATGCCGAAGTTGGGTACGATTAATCAAT 778
QY 824 TTGCTACAGTATGACATTAACAGTATTAATGATCTCGCAATTAATTTCCAAATATGATC 883
DB 779 TCCGTAGAGCAATGACTTTATATGTAATTAATTAAGTGGCACTATTTCCAAAGCTAATGAT 838
QY 884 CACGTAGTATCCATTAGCAAGTAAACGGAATTTGACTAGGAAAGTTTATACAGATCCAG 943
DB 839 CAAAAATGATCAATTAATAAACTAACGCCCACTTACAAAGAGATTAATACAGAGGCA 898
QY 944 TAGGGTTTACTGGGGGTATTAAGAAAGTGAGAGTACGACTTACCTTGGTATATCTTAATA 1003
DB 899 TTGGG---ACAGTACATCCGATCCCAAGTTTTCAGAGTACGACTGGTATTAATAATATAG 955
QY 1004 ATCAACCTTTACTGCTATGAGAAATTAAGCAAGAGAGCTCTTCTTATACCACTTGGC 1063
DB 956 CACCTTCTCTCTGTCATAGAGGCTGCTGTTGTTCAAAACCGCATCTAATCTGATTTTC 1015
QY 1064 TTAATGTAATTTTGTATATA---CAAGAGCTTAGGTAATATGCTGATGAGAAAT 1120
DB 1016 TAGAACAAGTAAATTTACAGCTTATTAAGTGAAGAGATTAACACTCAGATATAGATA 1075
QY 1121 TTGGGGAGGGCATACATTAGTTGAAATGAAATGATGTTGTAATTAATCAATTAATCT 1180

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DB 1076 TGTGGGAGAGCACTAAACCTAAGATTCGAAACATATAGAGGAAAGTTAAATATCTCAAC 1135
QY 1181 TTGTTAAACCTGATCTATTAATCTCTATTTCAATATTTTAAATTTTGGAACTTTGTTT 1240
DB 1136 AAGGATCTACTATTAATCTTCTATTAATCTCTGTAACATTTACCGTTCACTTCGAGAGCT 1195
QY 1241 TCAGATTAAGTACCTTCTCTGTAATATTTTATAGAGAAACAGAGGCTAATTAATTAATTA 1300
DB 1196 ATAGAGCTAATCATTTGCAAGGCTGAATCTATTTTAACTCAACCTGTTAAATGAGATAC 1255
QY 1301 CTAGAGTATAGAGCTGCAAGGATTTTATTAATCATCAAAATTAATTAATAGTACCTG 1360
DB 1256 CTAGGTTGATTTTCAATGAAATTTCTGACACATTCGATTCGATGTAATTTTC--- 1311
QY 1361 GATCTTTAAGATTAAGAGTGGCTGTAATCTTCCATCCCAACTATATTAATCAAGAAATAC 1420
DB 1312 --TATTTATCAGGGTATGCTGGAATTTGGAGCCGAATTAACAGATTCAGAAAAATGAAAT 1369
QY 1421 CAGAAAAAGATTAAGCCAAAGCAACCAAGAGATTTCAAGCATTAATTTATATATAT 1480
DB 1370 CACCTGAACCAACAGAGAGCCAAATTAATTAATCTTATAGTCAATATATCTCATATAG 1429
QY 1481 CAAATTTTATGACAGGCGAAGTATTCAGGGGTATTTGTAGCTTTTAACGTTGGTT 1540
DB 1430 -----GACTCATTTTCAAGCATCACATGTGAAAGCATTTGTAATTTCTT 1471
QY 1541 GGGCACAATACAGTATGATTCGTAATATATGCTTGAACAGATTAATTAATCAATTAATAG 1600
DB 1472 GAGCGATGCTAGTGAAGATCTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1531
QY 1601 ATGCACTTAAGGTT 1615
DB 1532 CATTAAGTAAAGCTT 1546

```

```

RESULT 10
US-08-460-570-1
; Sequence 1, Application US/08460570
; Patent No. 5965797
; GENERAL INFORMATION:
; APPLICANT: BLENK, ROBERT G.
; APPLICANT: ELY, SUSAN
; APPLICANT: TAILOR, RAVINDRA H.
; APPLICANT: TIPPETT, JANET M.
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U. S. A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,570
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,228
; FILING DATE: 09-MAY-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 218875/PS.35271/US/N

```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2965 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 US-08-460-570-1

Query Match 11.2%; Score 229.4; DB 2; Length 2965;
 Best Local Similarity 51.1%; Pred. No. 3.2e-46;
 Matches 713; Conservative 0; Mismatches 646; Indels 36; Gaps 6;

230 TTTTAAACGGGTATTAACAGGTAGAGCACTATCTTGGAAATTGAGGCTCCCTTGGCAA 289
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 290 GTCATCATTTGGAATTAATAGTAGGCTAATAGGATTTTATGAGGCA---GGGCGTATC 346
 593 GACAAAGTAGTACTCTTTATAGTTTATCTTAGGTAGCTATGAGCTTAAGGGGAAAAATC 652
 347 CATTTGAGCACTTAGTGTCTTGTGAGAGCTTATTAAGAAAAGTATAGATCAGCGTG 406
 653 AATGGGAATCTTATAGGAACATGAGATTAATTAATCAAAAATATCAACTATG 712
 407 TAAGAGAAATGCTCTTAGAGAGCTAGAGGTTTACAGGAAATTATGACTATATCAA 466
 713 CAGAAATTAAGCACTTACAGACTTGAAGATTAAGAGATGCGCTTAGCTGTACCATG 772
 467 CTAGACTGCAAGATGGCTAGTTAAAGAAATGATGCA---ATCGGAGGCACTAGTAA 523
 773 ATTCGCTTGAAGTGGGTTGGAATCTGTAATACACAGAGGCTAGAGGTTGTCAAGA 832
 524 CGCAGATGCAATGTGTTGATTAATCTTTTCGAAAAGATATGCCAAATTCAGAGAAAGAA 583
 833 GCCAATATATCGCATTAAGATTAATGTTGTTGTCGAAACCTACCTTTTGCAGTGTCTG 892
 584 ACTTTGAATTTTATTTGTTACAGTATATGCAAGCCGCGAAATTGCAATTTATTTAT 643
 893 GAGAGAGGTACCATTAATATCCATATATCCCAAGCTGCAAAATTTACATTTGTGTAT 952
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 764 ACCAGGTTTAAATCAATTAATCTGCTCAAAATGCTCAAGTTGGTGAAGCTTTAATAGT 823
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 944 TAGGGTTTACTGAGGATTAAGAAAGTGAAGGTAGCACTTACCTTGTATTAATCTTAATA 1003
 1253 TTGGG---ACAGTACATCCGATCCAAAGTTTCAAGTACGATGATTAATTAATGATG 1309
 1004 ATACAACTTATCTGATAGAGAAATTAACGCAAGACGACTCTTCTTATACCACTGGC 1063
 1310 CACCTTGTCTCTGCGATAGAGGCTGCTGTGTGAAACCGGCATCTACAGATTTTTC 1369
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1370 TAGAACAGTTACAAATTTACAGCTTATTAAGTCAGATGAGATACTCAGTATATGATA 1429
 1121 TTTGGGAGGCGATACATTAAGTTGAAATAATGATGTGCTGAAATTAACCATTAAT 1180
 1430 TGTGGGAGGACATTAATCTGAATTTCCGAACAAATAGAGGAACGTTAAATATCTCAAC 1489
 1181 TTGTAACCTGATTTCTATTAATCTCTAATTCATTAATTTTAATTTGCGAACCTTCTGTT 1240
 1490 AAGATCTACTAATTAATCTTATTAATTCCTGTAACTTACATTAACGCTTCTCGAGAGCT 1549
 1241 TCAATTTAGTCACTTGTCTGTAATATTTAGAGAGAACAGGCTTAATTAATTA 1300
 1550 ATGAGCTGATATTTGGCGAGGCTGATCTATTTTAATCTCAACCTGTTAAAGAGTAC 1609
 1301 CTAGCTAGTATGAGTCTGAGAGTTATTTTAATCATCAATTAATTAATTAATGTA 1360
 1610 CTAGGTTGATTTTCAATTTGAAATTTGTCACACATCCGATCGCATCTGATTAATTTTC--- 1665
 1361 GATCTTTAAGATACGAAGTCCCTGTAATCTTCATCCCACTAATTAATTAATTAATTA 1420
 1666--TATTAACAGGATATGCTGGAATTTGGACGCAATTAAGATTCAGAAATGAATTA 1723
 1421 CAGAAAGATTAAGCAAGACCAAGCAAGAGATTTCAAGCAATTAATTAATTAAT 1480
 1724 CACCTGAAGCAACAGACAGCCAAATTAATGAATCTTAATGATTAATTAATTAATTA 1783
 1481 CAAATTTGATGACGCGCAAGTATGATGAGGCTGATTTGTATCTTTTAACGTTGTT 1540
 1784-----GATCATTTCAAGCATCAATGTAAGAAAGATTTGATTAATTTCTT 1825
 1541 GGCACATACAGATATGATGATGTAATATGCTTGAACAGATTAATTAATTAATTA 1600
 1826 GAGCGATGCTAGTGAAGATGCTACAAATTAATTAATTAATTAATTAATTAATTA 1885
 1601 ATGCACTTAAGGTT 1615
 1886 CATTAGTAAAGCTT 1900

RESULT 11
 US-08-460-570-2
 Sequence 2, Application US/08460570
 Patent No. 5965797
 GENERAL INFORMATION:
 APPLICANT: BLENK, ROBERT G.
 APPLICANT: ELY, SUSAN
 APPLICANT: TAILOR, RAVINDRA H.
 APPLICANT: TIPPERT, JANET M.
 TITLE OF INVENTION: BACTERIAL GENES
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D. C.
 COUNTRY: U.S.A.
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,570
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/520,228
 FILING DATE: 09-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 8910624.9
 FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, Paul N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 218875/PS.35271/US/N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2965 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..2965
 US-08-460-570-2

Query Match 11.2%; Score 229.4; DB 2; Length 2965;
 Best Local Similarity 51.1%; Pred. No. 3.2e-46;
 Matches 713; Conservative 0; Mismatches 646; Indels 36; Gaps 6;

QY 230 TTTTAAAGGATTAACAGTGTAGGAGCTATCTTTCGAATTAGGGGTCCTTTGGCAA 289
 DB 533 TTCAAACAGGATTTGGATTGGCGGTAAATTAATTGGTACCTTAGGGGTTCTTTTGCA 592
 QY 290 GTCAATCATTTGGAAATATTAGTATAGGCTATATTTTATGGGCA--GGGCGTATC 346
 DB 593 GACAAAGTGTAGTCTTTATATGTTTATCTTAAAGTGTAGTATGCGCTTAAAGGAAAAATC 652
 QY 347 CATTTGAGCACTTATGTTCTTGTGAGAGCTTATTAAGAAAGTATAGTACAGGTG 406
 DB 653 AATGGAAATCTTTATGGAACATGTAGAGAGATTTATTCAAAAATTCACATTATG 712
 QY 407 TAAAGAAAAATGCTTTAGAGAGCTAGAGGTTTACAGGAATTTATGACTATATCAA 466
 DB 713 CAAAGAAATAAAGCACTTACAGACTTGAAGATTTAGAGATGCTTATGCTTACCATG 772
 QY 467 CTAGACTGCAAGCATGGCTATGTTTACAAAGATGATGACA--ATCGAGGGCACTAGTAA 523
 DB 773 ATTCGCTTGAAGATGGGTGTGAAATCGTATATACACAAAGGCTAGAGAGTGTCAAGA 832
 QY 524 CGCAGTATGCAATTTGTTGATTAATCTTTTGAAGAAAGATATGCCAAATTCAGAGAAAGAA 583
 DB 833 GCCAATATATCGCAATTAAGAAATGATGTTTCCTTCAAGAACTACTCTTTTGCAGTGTCTG 892
 QY 584 ACTTTGAAATTTTATTTGTTACAGATATATGACAAAGCCGCGAAATTTGCATTTAATTTAT 643
 DB 893 GAGAGAGGTACCATTTATTTACCATATATATGCCAAGCTGCAAAATTTTACATTTGTGCTAT 952
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 DB 953 TAAAGATGCTGATTTATTTTGGAAAGAGTGGGATTTATCATCTTCGAATTTTCAACAT 1012
 QY 704 AATTATACAGACTACAAAGAGCTGATTAGAGATTTAAAGATCAATTGATTAACATTTCTATA 763
 DB 1013 TTTATTAACCTTCAGTGAAGAGAGAGAGAGATTTCTTCAATTTGTTGAATTTGTTATA 1072
 QY 764 ACCAGGTTTAAATCAATTTTATGCTCAATGCTCAAGATTTGGGTAGGCTTTAATAGT 823
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 DB 1133 TCCGTAGAGACATGACTTTATGTTAGTACTAGATTAGTGCGCATATTTTCCAAAGCTATGATA 1192
 QY 884 CAGGTAGTATCAATTTAGCAGTAAAGAGGATTTGATAGGAGATTTATAGATCAG 943
 DB 1193 CACAAATGATCCAAATTAATTAATCAAGCCCACTTAAAGAGAGATATATACAGACGCAA 1252
 QY 944 TAGGTTTACTGGGTTATTAAGAAAGTGAAGTGAAGTCACTTACCTTGTATATCTTATA 1003

DB 1253 TTGGG---ACAGTACATCCGATCCAAAGTTTAAAGTATGCACTTGTATTAATTAATAG 1309
 QY 1004 ATACAACCTTTACTGCTATGAGAAATTAACGCAAGACAGAGTCTCTTTATACACTTGGC 1063
 DB 1310 CACCTTCGTTCTCTGCGATAGAGGCTGCTGTTGTTGGAACCCGCACTACTGATTTTC 1369
 QY 1064 TTAATGATATTTTGTATATA--CAAGACTCTAGATATATGTTGATGAGAAATA 1120
 DB 1370 TGAACAAAGTTACAAATTTACAGCTTATTTAATGATGAGTAACTCAGTATATGATA 1429
 QY 1121 TTTGGGAGGCACTATCATTTAGTGAAGAAATGAAATGATGGTCTGAAATTAACCATTA 1180
 DB 1430 TGTGGGAGAGACATTAACCTAGAAATCCGAAATAGAGAGAAAGTTAAATATCTCAAC 1489
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 DB 1490 AAGATCTACTAATCTTATTTATTCCTGTAACATTTACCGTTCACTTCCGAGAGCTCT 1549
 QY 1241 TCAGTATTAAGTCACTTGTCTGTATATTTAGAGAGAAACAGAGCTAATTAATTAATTA 1300
 DB 1550 ATAGGACTGATCATTTGGCAGGGCTGAATCTATTTTAACTCAACCTGTTAATGAGATAC 1609
 QY 1301 CTAGTCAATGAGCTGAGAGTATTTTATATATCATCAATTAATTAATTAATTAATTA 1360
 DB 1610 CTAGGCTGATTTTCAATTTGAAATTCGTCACATCCGATCGCATCTGAATATTTTC--- 1665
 QY 1361 GATCTTTAAGATACGAAGTGTCTGTATATTTAGAGAGAAACAGAGCTAATTAATTAATTA 1420
 DB 1666 --TATTTATCAGAGTATGCTGGAATTTGGAGCCCAATTAAGAGATTCAGAAATTAATTA 1723
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 DB 1724 CACCTGAACCAACAGGACAGCCAAATTAATTAATTAATTAATTAATTAATTAATTA 1783
 QY 1481 CAAATTTATGACAGGCGCAAGTATGTTGAGCGGATTTTGTACTTTTAACGTTGGTT 1540
 DB 1784 -----GACTCATTTACAGATCATCATGTGAAAGCATTTGATATTTCT 1825
 QY 1541 GGGCACAATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1600
 DB 1826 GAGCGCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1885
 QY 1601 ATGCACTTAAGGTT 1615
 DB 1886 CATTAATAAAGCTT 1900

RESULT 12
 US-08-286-870A-1
 ; Sequence 1, Application US/08286870A
 ; Patent No. 6063605
 ; GENERAL INFORMATION:
 ; APPLICANT: ELI, S
 ; APPLICANT: TAILOR, RH
 ; APPLICANT: TIPPERT, JM
 ; APPLICANT: BLENN, RG
 ; TITLE OF INVENTION: BACTERIAL GENES
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
 ; ADDRESSEE: Intellectual Property Group of
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30


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;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/286,870A
;
; FILING DATE: 05-AUG-1994
;
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/520228
;
; FILING DATE: 09-MAY-1990
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: GB 8910624.9
;
; FILING DATE: 09-MAY-1989
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: PAUL N. KOKULIS
;
; REGISTRATION NUMBER: 16,773
;
; REFERENCE/DOCKET NUMBER: 70608/220720
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202) 861-3000
;
; TELEFAX: (202) 822-0944
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2965 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: both
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: 1..2965
;
; US-08-286-870A-2
;
Query Match      11.2%; Score 229.4; DB 3; Length 2965;
Best Local Similarity 51.1%; Pred. No. 3.2e-46;
Matches 713; Conservative 0; Mismatches 646; Indels 36; Gaps 6;
;
QY 230 TTTTAA CGGGTATTA CAGTGA GGCCTA CTACTT TCGAAT TTAAGGGG TCCTTTGG CAA 289
DB 533 TTCAAACAGTAT TGGATT GCGGGT AAAATAC TGTGTA CCTAGG GGTTCCTTTGG CAG 592
QY 290 GTCAATCATTTT GGAATTA TTAAGTA AGGCTA ATAGGT ATTTTATG GGC---GGCCTG ATC 346
DB 593 GACAAGTAGCTAC TCTTATG TTTATCTT AGGTGAG CTATGCG CTTAAGGGG AAAAATC 652
QY 347 CATTTAGAGCACT TATAGT GTTCTT TGAAGAG CTTATTA GAAAGAT TATGATC ACGGTG 406
DB 653 AATGGAAATCTT TATGAA CAGTGA AGATTT ATTAATC AAAAAAT ATCAACTT ATG 712
QY 407 TTAAGAAAAATG CTCTTA GAGCTA GAGCTTA CAGGAA TTATGA CTAATATC AAT 466
DB 713 CAAGAAATAAGCA CTTACAG ACTTGA AGAGAT TTAGGA GATGCTT AAGCTGATC ATG 772
QY 467 CTAGACTGCA GAGATG GCTATG TTAACA GATATGA CA---ATCG AGGGCA CTATG TAA 523
DB 773 ATTCGCTTGA AATGGG GTTGA AATCGT ATAAACA CAAAGG CTTAGGA GTGTGCA AGA 832
QY 524 CGAGATGAGCA ATTTGTA TAACTTTT TCGAAA GAATATG CCAAAAT TCAAGAAA AGA 583
DB 833 GCCAATATATCG CATTGA AATGATG TCGTCA GAAACAT CTTCTTTG CAGTGTCTG 892
QY 584 ACTTTGAAATTTT ATTTGTT ACCAGT ATATG CACA GACCGG CCAATTTG CATTATTTTAT 643
DB 893 GAGAGAGAGTAC ATTTAT TTAACCAT ATATG CCAAGCTG CAAATTTT AATTTTGTCTAT 952
QY 644 TTAAGATGCTGAT TATATTT TGAACA CAGTGC AATTAG GTATG ATGAAAT TCGTGATA 703
DB 953 TTAAGATGCTAT TATTTT TGAAGA AAGAGT GGGATTA TATCAT CTCGAA AATTTCAACAT 1012
QY 704 ATATATTCAGAC TACACA GAGCTG ATTAAGA AATATTA AGTCTT GTATATTA ACCTTTAT 763
DB 1013 TTATATACCGTCA AGTCGA ACAGCA GAGATTA ATTCCTT ACATGT GTGAAAT TGGTATA 1072

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QY 764 ACCAGGTTTAA TCAATTTA TCGCTCA AATCTCA AGTTGG GTAGCTTATATAGT 823
DB 1073 GCACAGGTCTAA TAACTTGA GGGGTAC AAATGCCC AAAAGTTGG GTATACGATATATCAAT 1132
QY 824 TTGCTACAGTATG AATTAACA GTATGATG TCGCAATATTA TTTCCAACTATGATC 883
DB 1133 TCCGTAGACATG AATTTAATG GATCTGA ATTTAGTGG CACTATTTTCCAA GCTATGATA 1192
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DB 1310 CACCTTGTCTCTG CATTAGAG GGTGCTGTGTTG TGAACCCG CACTTACTGATTTTTC 1369
QY 1064 TTATGCTATTTT TGTATATA ---CAAGACTCTAGTATATATGCTGATGTAGAAATA 1120
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DB 1430 TGTGGGAGGACA TAAACTGA AATTCGAA CATAAGAGGAAGTTAAATATCTCAACAC 1489
QY 1181 TTGCTAAAATGAT TCTATATTA CTCCATTA CAATATTTTATTTGGGAACTTTCGTTT 1240
DB 1490 AAGGATCTACTA TATCTCTATTAATCTGTAACATTA CCGTCACTTCTCGAGACGTCT 1549
QY 1241 TCAGATATAGTCA CTCTGCTGTA TATATTTA GAGAAACAGAGGCTAAATATATATTA 1300
DB 1550 ATAGACTGATAT CATTTGGCAG GGTGATCTATTTTAACTCA ACTGTTATGAGATAC 1609
QY 1301 CTATGATGATGAG TCTCGAGAT TATTTTAATCATCA AATATATATATATATGTA CTTG 1360
DB 1610 CTAGGGTATATTTT CATGGA AATTCGTCA CACTCGCATCGCATCTGATTAATTTTC--- 1665
QY 1361 GATCTTTAAGATACGA AGTGCCTGCTAATCTTCCATCCCAACTATATATATCAAGATTTAC 1420
DB 1666 --TATATATCAGGGATATGCTGA AATGGACGCAATTA CAGATTAAGAAAATGAAATTTAC 1723
QY 1421 CAGAAAGATATA GCAACCAAGC CAAAGCAGAGATTTCCAGCCTATGATTAATCTTATATAT 1480
DB 1724 CACCTGAACACA CAGACAGC CAAATTAATGAA TCTTATAGTCA TATATATCTCATATAG 1783
QY 1481 CAAATTTGATGCA CGGCGAAGT AGTTCA GCGCGTATGTTAGTCTTTTAACTGTTGGTT 1540
DB 1784 -----GACTCATTTCA GCAATCA CATGTGA AAGCATTTGATATATTTCTT 1825
QY 1541 GGGCACAATACA GTATGATGCTGTAATATATGCTTCTTGA ACCAGATTAATAATCAATAATG 1600
DB 1826 GGAACGATGTGTGTCAGATCGTCA AATTAATCAATTAAGG CCAATATACATTAA CAAATATAC 1885
QY 1601 ATGCAAGTTAAAGTTT 1615
DB 1886 CATTAGTAAAGCTT 1900

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; RESULT 14
;
; US-08-448-170-7
;
; Sequence 7, Application US/08448170
;
; Patent No. 5723758
;
; GENERAL INFORMATION:
;
; APPLICANT: Payne, Jewel
;
; APPLICANT: Cummings, David A.
;
; APPLICANT: Cannon, Raymond J. C.
;
; APPLICANT: Narva, Kenneth E.
;
; APPLICANT: Steiman, Steve
;
; TITLE OF INVENTION: No. 5723758e1 Bacillus thuringiensis Isolate Denoted

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TITLE OF INVENTION: B.c. PS158C2, Active Against Lepidopteran Pests, and Genes
 TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David R. Salimanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/448,170
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,902
 FILING DATE: 01-JUNE-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/759,247
 FILING DATE: 13-SEPT-1991
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Salimanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: M/S 102D.C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 375-8100
 TELEFAX: (904) 372-5800
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3684 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-448-170-7

Query Match 10.9%; Score 223.6; DB 2; Length 3684;
 Best Local Similarity 51.9%; Pred. No. 9.1e-45;
 Matches 655; Conservative 0; Mismatches 589; Indels 18; Gaps 6;

227 CTGTTTAAAGGGATTTACAGTGAAGGACTATCTTTCGAATTTAGGGGTCCTTTGG 286
 164 CAGTCCAAACGGGATTTAATACATAGCTGTGAATTAAGGTGATTAAGGGTACCGTTTG 223
 287 CAAATCAATCTTTGGAAATTAATTAAGGCTAATAGGATTTTATGCGCA--GGGCTG 343
 224 CTGGACAATATAGCTAGTTTATATAGTTTCTGTGTGTGAATTAATGCCCCGGGCAAG 283
 344 ATCCATTTGAAGCACTTATAGGCTTCTGTGAAGGCTTATTAAGAAAGATATGATCAGC 403
 284 ATCTTGGGAATTTTCTTGAACATGTCGACAACTATTAACAAAGTAACAGAAA 343
 404 GTGTAAAGAAAATGCTCTTGAAGAGCTAGAGGTTTACAGGAATTAATGAGACTATATC 463
 344 ATACTAGGGATTAAGGCTCTTGTCTCGATTAACAAGTTTGAAGAAATCTTTAGAGCTATC 403
 464 AAACCTGACTGCAGCATGGCTGTGTAACAAGATGATG--ACAATCGAGGGCACTAG 520
 404 AACAGTCACTTGAAGATGGCTGAAGAAACCGTATGATGACAGAGCAAGATGTTCTTT 463
 521 TAACGAGTATGGAATTTGATTAATCTTTTTCGAAAAGATATGCCAAAATTCAGAGAA 580
 464 ATACCCAAATATATAGCTTGAAGATTTGATTTCTTAATGCGATGCGCTTTTGCAATTA 523
 581 GAAACTTGAATTTTATTTGTTACAGATATATGACAAAGCCGGAATTTGCAATTAATTT 640

524 GAAACCAAGAAATTCATTAATATATATATATATATATATATATATATATATATATAT 583
 641 TATTAAGAGATGCTGATTAATTTTGAAGCAAGTGGCAATTAAGGATGATGAATTCGTG 700
 584 TATTAAGAGATGCTGCTCTTTTGTGATGAATTTGGGCTTAATCCCAAGAAATTCAC 643
 701 ATAAATATATACAGTACCAAGACGATTAAGAAATTAAGATATATATATATATATATAT 760
 644 GTTATATATAGCCCAAGTGAAGAAAACGAGAAATATCTGATTAATTTGGCAAGATGT 703
 761 ATTAACCAAGGTTTAAATCAATTTAATGCTCAATGCTCAAGATTTGGGTAGCTTTATA 820
 704 ATAAATCGGGTTTAAATTAATTTGAAGGGAACAATGCTGAAGTTGGTTCCGATATATC 763
 821 GGTTCGTACAGATATGACATTAACATTAATGATCTCGCAATATTAATTTCCAACTATG 880
 764 AATTCGTAGAGCTTAACGCTTAGAGATTAATTAATCTAGTGGCAATTTCCCAAGCTATG 823
 881 ATCCAGTATGATATCCATTAAGCAGTAAACGGAATTTGACTAGGAAATTTATACAGATC 940
 824 ACAAGGCTGTTTATCCAAATGAATACAGATGCTCAATTAACAGAAATTTATACAGATC 883
 941 CAGTAGGCTTACTGGGATTTGAAGAAAGTGAAGTGAAGTACCTTCCTTGTATATCTTA 1000
 884 CAATTTGGGAAACAAATGCACTTCAGGATTTGCAAGTACGAA--TTGGTTTAAATATA 940
 1001 ATAAATCAACCTTACTGCTATGAGAAATAATACGCAAGACGCTTCCTTATACACTT 1060
 941 ATGACCATGCTTTTCTGCAATAGAGCTGCTTTATAGGCTTCGCACTTCTGAT 1000
 1061 GGC--TTAATCGTATTTTGTATATACAGACCTAGGTAATATGATGATGAGAA 1117
 1001 TTCCAGAACAGCTTAATCAATTTTCAAGGATTAAGTGAATGATGATTAATCAATATGA 1060
 1118 ATATTTGGGAGGGCACTAATTAAGTGAAGAAATGATGCTTGAATATACCATTA 1177
 1061 ATTAATGAGGAGGACATGACCTTAATGCGAACAATTAAGGGGCTAATTAAGTACCTCGA 1120
 1178 ACTTGTAAATCTGATTAATCTTACTTCTTATTCGAATTTTATTTTGGGAACTTTCTG 1237
 1121 CACAGCAATATCAATTAATCTTATTAATCTTGAATTAATCAATTAATCAATCTGAGACG 1180
 1238 TTTTCAATTTAGTCACTTCTGATTAATTTATTTAGAGGAAACAGAGGCTAATATATA 1297
 1181 TTTATGAACAGATCAATTTTGAAGGATTAATTAATCTTCAATCTCCTGATATGAG 1240
 1298 TTAATGATCAATGAGTCTCGAGATTAATTTTAAATCAATCAATTAATTAATGATAC 1357
 1241 TACCTTGGGCTAGATTTAATTTGAAGAAATCCCTGAAT--TCTTTAGAGTACCTTC 1297
 1358 CTGATCTTTAAGATACGAAGTCCCTGATATTTCCATCCCAATATATATATCAGAAT 1417
 1298 TCTATCTATATAGGATTAATCTGAGTGGGACAACTATTTGA--TTCCGAATCGAAT 1354
 1418 TACCAGAAAGATTAAGCAACCAAGCAAGAGATTTACGCCATATATATTTTATA 1477
 1355 TACCACCAAGAAACAGAAACGCAATTAATTAATCTTAAGTCAATATATATTA 1414
 1478 TA 1479
 1415 TA 1416

RESULT 15
 US-08-961-803-5
 Sequence 5, Application US/08961803
 Patent No. 6150589
 GENERAL INFORMATION:
 APPLICANT: Payne, Jewel
 APPLICANT: Cummings, David A.
 APPLICANT: Cannon, Raymond J.C.
 APPLICANT: Narva, Kenneth E.
 APPLICANT: Stelman, Steve

TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PSI5862, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: M/S 102DCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-961-803-5

Query Match 10.9%; Score 223.6; DB 3; Length 3684;
Best Local Similarity 51.9%; Pred. No. 9.1e-45;
Matches 655; Conservative 0; Mismatches 589; Indels 18; Gaps 6;

227 CTTCTTTAAGGGATTAAGAGTGAAGCTACTTCTTGAATTTAGGGGCTCCCTTTGG 286
164 CACTCCAAAGGGATTAAACATGCTGTGAATACAGTGTATTAAGGGTACCGTTTG 223
287 CAAGTCATCATTTGGAATTAATTAGTGGCTAAATAGTATTTTATGGGCA---GGGCTG 343
224 CTGAGACAAATAGCTAGTTTATAGTTTCTGTGTGTAATTAAGCCCGGGCGAG 283
344 ATTCATTGGAAGCACTTAGGCTTCTGTGTAAGAGCTTATTAAGAAAAGTATGATCAGC 403
284 ATCTTGGGAAATTTCTCTAGAACATGTGAAACAACTTATAGCAACAAGTAAAGAAA 343
404 GTGTAGAGAAATGCTCTTAGAGAGCTAGAGTTTACAGGGAATTAATGACTATATC 463
344 ATACTAGGAGTACGGCTTCTGCTGATTAACAGGTTTAGAAATTCCTTTAGAGCTATC 403
464 AAACAGACTGCAAGCATGGCTAGTTTACAGAAATGATG---ACAATCGAGGCGACTAG 520
404 AACAGTCACTTGAAATGGCTAGAGAAAACGTGATGATGCAAGAACGAAGTGTCTTT 463
521 TAAAGCATGATGCAATTTGTTATTAATTTTCGAAAAAGAAATATGCCAAATTCAGAGAA 580

464 ATACCAATATATAGCTTAGAATTTCTTATATGAGGCGGCTTTGCAATTA 523
581 GAAACTTTGAAATTTATTTGTTTACAGTATATGACAAAGCCGGAATTTGATTTAATTT 640
524 GAAACCAAGATGCTCATTTATTAATGATATGCTCAAGCTGCAATTTTACACTTAT 583
641 TATTAAGATGCTGATTAATTTTGGAGCAAGTGCATTTAGGTATGATGAATTCGTG 700
584 TATTAAGATGCTGCTCTTTTGGTATGAAATTTGGGCTTACATCCCAAGAAATTCAC 643
701 ATATATATATGACATGACAAAGACTGATTAAGAAATATAAGTCAATGATTAACATTC 760
644 GTTATATATAGCGCCAAAGTGAAGAAAAAGAGAAATATCTGATTAATGCGCAAGTGT 703
761 ATACAGGCTTTAATCAATTTAATGCTCAAAATGCTCAAGATTTGGTGAAGCTTTAATA 820
704 ATATACGGGTTTAAATTAATTTGAGAGGACAAATGCTGAAGTTGGTGGATATATC 763
821 GGTTCGTACAGATATGACATTAACATTAATGATCTCGCAATATTTTCCAACTATG 880
764 AATTCGTAGAGCTTAACGCTAGAGATTAATGATCTAGGCGACTATCCCAAGCTATG 823
881 ATCCAGTATGATATCCATTAAGCAATTAAGAAACGGAATTTGCTAGGAACTTATACGATC 940
824 ACACGGGTATTAATCAATGAATATCAAGTCTCAATTAACAAAGAAATTTATACGATC 883
941 CAGTAGGCTTTAATGAGGATTTAGAAATGAGAGTGAAGCTTAACCTGTATATATCTTA 1000
884 CATTTGGAGAACAAATGACACCTGAGATTTGCAAGTACGAA---TTGGTTAATATATA 940
1001 ATATATCAACTTTTACTGCTATGGAATAATGACGAAGACGCTCTTCTTATACACTT 1060
941 ATGACCATGCTGTTTCTGCATATAGAGCTGCGCTTATTTAGGCTCTCGCATCTATGAT 1000
1061 GGC---TTAATGATATTTTGTATATACAGGACTAGGATATATGTCATGTGAGAA 1117
1001 TTCCAGAACGCTTAACAATTTTCAAGCTATTAAGTGAAGATTAATCTCAATATATGA 1060
1118 ATATTTGGGAGGACATTAATTAATGTAATGGAATGATGTTCTGAATTAACCATTA 1177
1061 ATTACTGGGTGGGACATTAAGCTTAATGCGAACAATTAAGGGGCTATTAAGTACCGA 1120
1178 ACTTTGTAATACTGATTTCTATTAATCTCTATTAATTTAATTTTCGGAACCTTTCTG 1237
1121 CACACGAAATATCAATTAATCTTATTAATCTGTAACATTAACATTCACATCTCGAGACG 1180
1238 TTTTCAGTATGAGTCACTTGTCTGATATATTTAGAGGAAACAGAGGCTAATATATA 1297
1181 TTTATGAACAGATATTTGACAGGATTAATTAATTAATCTTCTTAATCTCTGTAATGAG 1240
1298 TTACTGTCAGTATGAGTCTCGAGAGTTATTTTATATCATCAATTAATTAATGATAC 1357
1241 TACTTTGGGCTGATTTAATTTGAGAAATCCCTGAAAT---TCTCTTAAGAGTACCTTC 1297
1358 CTGGAATCTTAAGATATGAAAGTCTGCTGATTAATTTTCAATCCAACTATATTAAT 1417
1298 TCTATCTATAGGATTAATCTGAGTGGGACACAACTAATTTGA---TTGAAATCTGAAT 1354
1418 TACCAAGAAAGATTAAGCCAAAGCAAGCAAGGAGATTTACCCATPAATTTATATATA 1477
1355 TACCAACAGAAACAAAGAAAGCAAAATTAATTAATTTAAGTCAATGATTAATTAATA 1414
1478 TA 1479
1415 TA 1416

Search completed: December 24, 2005, 18:55:45
Job time : 401 secs


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Db 10 AATATCAAAATGATATGAAATTAATGATGACACCTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAGAGTATCCACTAGCAAAAAGATCCAAATGACTATGCGAAACGAACTAT 132
Db 67 GATTCTAACGATACCTTTTGGAATGAGCCCAACAAATGCGTACAAAATATGATAT 126
Qy 133 AAGAAATGCTAAATATGATGATTCAAATATACAAATTAATGATATAGACAGTAT 192
Db 127 AAGATTAATTAATAATGCTGCGGGAATGCTAGTGAATACCTGGTCA----- 177
Qy 193 TCTAGCCCTGAACTGCTTTAACTGACGAGATGCTGTTTAAAGGATATTAAGTGA 252
Db 178 -----CCTGAAGTACTTGTATACCGCAAGATGCAAGATGAGCCGCAATGTATAGTA 231
Qy 253 GGGACTATACCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAAGT 312
Db 232 GGTAAATTAATCTACAGTTTAAAGGGTCCCATTTGTTGGCCGATAGTGAATCTTTATCT 291
Qy 313 AGGCTAATAGTATTTTATGCGCAGGGCCTGA-----TCCATTTGAAAGCATTTATGTT 366
Db 292 CAATTAATGATATTTCTGTGCGCTTCAGGGGAAAAGATGCAATGGGAAATTTTATGAA 351
Qy 367 CTGTGTAAGAGCTTATTAAGAAAAGTATGATCAGCGTGTAAAGAAAATGCTCTTA 426
Db 352 CAAGTGAAGAACTCATTTATCAAAAATGACAAATATGCAAGATTAAGGCGCTTTCG 411
Qy 427 GAGCTAAGAGGTTTACAGGGAATTAATGAGACTATATCAAACTAGACTGCAAGCATGCTA 486
Db 412 GAATTTGAAGATTTAGTATATATTAACCAATTAATCTAATCTGCGCTTGAAGAAATGGA 471
Qy 487 GTTAACAGATGATGACATTCGAGGGCACTAGT---AACGAGATATGCAATTTGTTAT 543
Db 472 GAAATATCCAAATGCTTCAGAGGCTTACGAGATGAGGAAATGCAATTTGAAATCCGAT 531
Qy 544 AACTTTTGAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTATTTGTTA 603
Db 532 AGTTTATTTACGCAATATATATGCAATCTTTTAAAGTGAACAAATTTGAATGCAATTCCT 591
Qy 604 CCAGTATATGACAAAGCGCGCAATTTGCAATTTATTTAAGAGATGCTATTTATTT 663
Db 592 ACTGTATATGCAATGCGAGCCAACTTCAATTTACTGTATTTAAAGAGCGGCTCAATTTT 651
Qy 664 GGAGCAGATGCGAATTAAGTGTATGTAATTCGTATATTAATATACACTACAAAGA 723
Db 652 GAGGAAGAAATGGGAGTGTGCAACAACTACTATTAATATGATATGCTCAATAGAA 711
Qy 724 CTGATTAAGAAATATAAGATCTTGTATTAACATTTCTATACAGAGGTTTAAATCAATT 783
Db 712 CTTACTGCAAGAAATTTCTGATCACTGTATAGTGTATGAAACTGGTTTACGAAATTA 771
Qy 784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTGTACAGATATGACATTA 843
Db 772 AAGGCAAGAGCGCTTAACATATGAGTTGACTATTAACCAATTCGTTAGAGAAATGACAT 831
Qy 844 ACAGTATTAATCTGCAATATTAATTTCCAACTATGATCCAGTATGATATTCATTAACA 903
Db 832 GCGGTTTATGATTTGTGTGATTAATTCGCAAAATTAAGACACAGCAGTATCCCAATGGA 891
Qy 904 GTAAAAACGGAATTAAGTGAAGATTTATACAGATCCAGTAGG 947
Db 892 ACGAAAGCACAACTAACAGGGAATATATACAGATCCAGTGG 935
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RESULT 2
US-11-108-389-11

Sequence 11, Application US/11108389
Publication No. US2005026118A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu

```
APPLICANT: Billy Fred McClutchen  
APPLICANT: James K. Presnall  
APPLICANT: James F.H. Wong  
APPLICANT: Cao-Guo Yu  
TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal  
FILE REFERENCE: 35718/291049  
CURRENT APPLICATION NUMBER: US/11/108,389  
CURRENT FILING DATE: 2005-04-18  
PRIOR APPLICATION NUMBER: 60/391,786  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: 60/460,787  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: 10/606,320  
PRIOR FILING DATE: 2003-06-25  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: PaetsSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 2010  
TYPE: DNA  
ORGANISM: Bacillus thuringiensis (truncated)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(2010)  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: 1218-1A  
US-11-108-389-11
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Query Match 11.5%; Score 235.6; DB 7; Length 2010;
Best Local Similarity 56.5%; Pred. No. 7.5e-45;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

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Qy 13 AAAAAAAGAAATGAAATGTTGATGCTTTACGAATCAACTTAATATGCTATAT 72
Db 10 AATATCAAAATGAAATTAATGATGAGACCTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAGAGTATCCACTAGCAAAAAGATCCAAATGACTATGCGAAACGAACTAT 132
Db 67 GATTCTAACGATACCTTTTGGAATGAGCCCAACAAATGCGTACAAAATATGATAT 126
Qy 133 AAGAAATGCTAAATATGATGATTCAAATATACAAATTAATGATATAGACAGTAT 192
Db 127 AAGATTAATTAATAATGCTGCGGGAATGCTAGTGAATACCTGGTCA----- 177
Qy 193 TCTAGCCCTGAACTGCTTTAACTGACGAGATGCTGTTTAAAGGATATTAAGTGA 252
Db 178 -----CCTGAAGTACTTGTATACCGCAAGATGCAAGATGAGCCGCAATGTATAGTA 231
Qy 253 GGGACTATACCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAAGT 312
Db 232 GGTAAATTAATCTACAGTTTAAAGGGTCCCATTTGTTGGCCGATAGTGAATCTTTATCT 291
Qy 313 AGGCTAATAGTATTTTATGCGCAGGGCCTGA-----TCCATTTGAAAGCATTTATGTT 366
Db 292 CAATTAATGATATTTCTGTGCGCTTCAGGGGAAAAGATGCAATGGGAAATTTTATGAA 351
Qy 367 CTGTGTAAGAGCTTATTAAGAAAAGTATGATCAGCGTGTAAAGAAAATGCTCTTA 426
Db 352 CAAGTGAAGAACTCATTTATCAAAAATGACAAATATGCAAGATTAAGGCGCTTTCG 411
Qy 427 GAGCTAAGAGGTTTACAGGGAATTAAGACTATATCAAACTAGACTGCAAGCATGCTA 486
Db 412 GAATTTGAAGATTTAGTATATTAATTAACCAATTAATCTAATCTGCGCTTGAAGAAATGGA 471
Qy 487 GTTAACAGATGATGACATTCGAGGGCACTAGT---AACGAGTATGCAATTTGTTAT 543
Db 472 GAAATATCCAAATGCTTCAGAGGCTTACGAGATGAGGAAATGCAATTTGAAATCCGAT 531
Qy 544 AACTTTTGAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTATTTGTTA 603
Db 532 AGTTTATTTACCAATATATGCAATCTTTTAAAGTGAACAAATTTGAATGCAATTCCT 591
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QY 604 CCAGTATATGCACAGCCGGAAATTTGCAATTAATTTAAGAGATGCTGATTTT 663
DB 592 ACTGTATATGCATGAGGCAACCTTCAATTTGATTAATTAAGAGCGGTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTATGATGAATAATTCGTATTAATTAATCACTACAGCA 723
DB 652 GGAGAAAGATGGGATGATGCAACAATCTATTATTAATCTATTATGATCGTCAATGAA 711
QY 724 CTGATTAAGAAATTAAGATTCATGATTAATCAATCTATTAACAGGCTTAAATCAATTT 783
DB 712 CTTACTGCAAAATTTCTGATCACTGTGAAGGTGATGAACCTGTTTAAAGAAATTA 771
QY 784 AATCGCTCAAAATGCTCAAGATGGGTGAGCTTTAATAGTTTGTGACAGATATGACATTA 843
DB 772 AAGGCAAGGCGCTTAACATAGGTTGATTAACCAATTCGTAGAGAAATGACACTG 831
QY 844 ACAGTATTAGATCTCGCAATATTAATTTCCAACTAGATCCAGTAGATTCATTAAGA 903
DB 832 GCGGTTTATGATGTGTGATTAATTCCTCAATATTAACACAGCAGTACCAATGAA 891
QY 904 GTAAAAACGAATTGACTAGGAAATTAATACAGATCCAGTAGG 947
DB 892 ACGAAAGCACACTAACAGGAAATTAATACAGATCCAGTAGG 935

RESULT 3
US-11-058-727-1
; Sequence 1, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnell
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Acclivity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CRY1218-1
; US-11-058-727-1

Query Match 11.54; Score 235.6; DB 7; Length 3621;
Best Local Similarity 56.54; Pred. No. 9.2e-45;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATGAATGTTGATGCTTTAGCAATCACTTAATATGCTAAT 72
DB 10 AATTAATCAAAATGAATTAATGATGACGACCTCTTA---CTTGTATCAAT 66

QY 73 TGTATCCAAAGTATCCATAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
DB 67 GATTTCAGAGATACCTTTTGGAAATGAGCACAACATCGGTACAAAATATGATTAAT 126
QY 133 AAGAAATGCTAAATATGTGTATTCGAATTAACAATTAATTAATGATATAGCAGTAT 192
DB 127 AAGATTAATTAATAAATGTCTGGGAAATGATGAAATACCTGCTTCA----- 177
QY 193 TCTAGCCCTGAACTGTTTAAGTATGATGATGCTGTTTAAGGCTATTAACGTGA 252
DB 178 -----CTGAATTAATCTGTTAGCGACAGATGACGTAAAGCCGCAATTAATATGA 231
QY 253 GGGACTATACCTTTCGAATTTAGGGGTCCCTTTGGCAAGTCAATTTGGAATTAATAGT 312
DB 232 GTTAATTAATCAAGTTTAAAGGATCCCATTTGTTGGCCGATGATGATCTTTAATCT 291
QY 313 AGGCTAATAGTATTTTATGCGAGGCGCTGA-----TCAATTTAGACATTAATGTT 366
DB 292 CAATTAATGATATTCGTGGCCTTCAGGGGAAAGATCAATGGAATTTTATGGA 351
QY 367 CTGTTGAAGCTTTAATTAAGAAATTAATGATCAAGCTGTAAGAAATGCTTTAGA 426
DB 352 CAAGTAAAGAACTCAATTAATCAAAATTAAGCAAAATTAAGCAATTAAGCAATTAAG 411
QY 427 GAGCTAAGAGTTTACAGGAAATTAATGATGATCAATCAATCAATCAATCAATCAATCA 486
DB 412 GAATTAAGAAATTAAGTATTAATTAATCAATTAATTAATCAATCAATCAATCAATCA 471
QY 487 GTTAACAGAAATGATGACAAATCGAGGCGCACTAGT---AAGCAATTAAGCAATTTGAT 543
DB 472 GAAATTCAAATGTTTCAAGAGCTTAAGAGATGATGGAATGATTAATGAAATCCGAT 531
QY 544 AACTTTTGAAGAAATTAATGCAAAATTAAGAAAGAACTTGAATTTATTTCTTA 603
DB 532 AGTTTATTAACGCAATTAATGATGATCTTTTAAAGTGAACAAATTTGAATGATTCCTT 591
QY 604 CCAGTATTAAGCAAGGCGGCAATTTGCAATTTAATTTAATTAAGATGCTGATTAATTT 663
DB 592 ACTGTATATGCATGAGGCAACCTTCAATTTCTGTATTAAGACGCGTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTATGATGAATAATTCGTATTAATTAATCACTACAGCA 723
DB 652 GGAGAAATGGGATGATGCAACAATCTATTATTAATGATGATGCTCAATGAA 711
QY 724 CTGATTAAGAAATTAAGATCTTGTATTAATCTTAATCAAGGCTTAAATCAATTT 783
DB 712 CTTACTGCAAAATTTCTGATCACTGTGAAGGTGATGAACCTGTTTAAAGAAATTA 771
QY 784 AATCGCTCAAAATGCTCAAGATGGGTGAGCTTTAATAGTTTGTGACAGATATGACATTA 843
DB 772 AAGGCAAGGCGCTTAACATAGGTTGATTAACCAATTCGTAGAGAAATGACACTG 831
QY 844 ACAGTATTAGATCTCGCAATATTAATTTCCAACTAGATCCAGTAGATTCATTAAGA 903
DB 832 GCGGTTTATGATGTGTGATTAATTCCTCAATATTAAGACAGCAGTACCAATGAA 891
QY 904 GTAAAAACGAATTGACTAGGAAATTAATTAACAGATCCAGTAGG 947
DB 892 ACGAAAGCACACTAACAGGAAATTAATACAGATCCAGTAGG 935

RESULT 4
US-11-108-389-1
; Sequence 1, Application US/1108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen


```

QY 133 AAGAAATGCTAAATATGTGATTCAAATACAAATTTATTTGGATATATAGCACTAT 192
Db 857 AAGATATATTTAAAAATGTCTGGCGGAAATCTGATGAATACCTGGTCA----- 907
QY 193 TCTAGCCCTGAAGTCTCTTAAGTGTACGAGATCTCTTTTAAACGGGTATTAACAGTGA 252
Db 908 -----CCTAAGATCTGTGTAGCGGACAGATCAGCTAAGCGGCAATTTGAATATGTA 961
QY 253 GGGACTATCTTGGAAATTTAGGGGTCCTTTGGCAGTCAATCAATTTGGAATTAATAGT 312
Db 962 GGTAAATTAATAGTTAGGTTAGGGGTCCTCAATTTTGGCCGATGATGATCTTAACT 1021
QY 313 AGGCTAATAGTATTTTATGGGCGGCGCTGA-----TCCATTTGAAGCACTATGCTT 366
Db 1022 CAATTAATGATATCTGTGGCCCTTCAAGGGAAGAGTCAATGGGAAATTTTATATGAA 1081
QY 367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCGGTAGAGAAAATGCTTTAGA 426
Db 1082 CAAGTAAAGAACTCATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTTCG 1141
QY 427 GAGCTAAGATTTACAGGGAATATAGACTATATCAATCAATGCAAGCAAGTGGCTA 486
Db 1142 GAATTAAGAAATTAAGGTAAATTAATACCAATATATCTAATCTGCTTGAAGATGGAA 1201
QY 487 GTTAACAAAGATGATGACAAATCGGAGGGCACTAGT---AAGCAGATATGCAATTTGAT 543
Db 1202 GAAATTCAAATATGTTCAAGAGCTTACGAGATGCGGAAATGCAATTTGAATCTGGAT 1261
QY 544 AACTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTA 603
Db 1262 AGTTATATTTACGCAATATATGCGCATCTTTAGAGTGAACAATTTTGAAGTACATTCCT 1321
QY 604 CCAATATATGCAAGAGCGGGAATTTGCAATTTATTTTAAAGATGCTGATATTTT 663
Db 1322 ACTGTAATATGCAATGAGGCAACCTTCATTTACTGTTATTAAGAGCGGTCATTTT 1381
QY 664 GGAGCAGTGGCAATTAGGTGATGATGAATTCGTGATATATATACACTACAGGA 723
Db 1382 GGAGAAATATGGGATGATGATCAACACTATTTATTAATCTATTTATGCTCAATGAAA 1441
QY 724 CTGATTAAGAAATATTAAGATTCATTTGTAATCAATTTCTAATCAAGGTTTAAATCAAT 783
Db 1442 CTTACGCAAGAAATATCTGATCACTGTGTAAGTGTATGAATCTGTTTAAAGAAATTA 1501
QY 784 AATCGCTCAATATGCTCAAGTATGGGTGAGCTTTAATAGTTTGTACAGATATGACATTA 843
Db 1502 AAGGCAAGCGGCTTAAACAAATGGGTGACTATTAACCAATTCGATAGAGAAATGACACTG 1561
QY 844 ACAGTATTAATCTCGCAATATTTATTCAAACTATGATCAAGTAGATATTCATTAGCA 903
Db 1562 GCGGTTTATATGTTGTTGCTATTTATTCCTCAATTTATATACACAGCACTTACCAATGAA 1621
QY 904 GTAAAAACGGAATTTGACTAGGGAAGTTTATATACAGATCCAGTAGG 947
Db 1622 ACGAAAGCAACAATTAACAGGGAAGTATATACAGATCACTGGG 1665

```

```

RESULT 6
US-11-108-389-17
; Sequence 17, Application US/11108389
; Publication No. US2005026188A1
; GENERAL INFORMATION:
; APPLICANT: Andre K. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Frensdall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

```

```

; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ. ID NOS: 134
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ. ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17

Query Match 11.5%; Score 235.6; DB 7; Length 4874;
Best Local Similarity 56.5%; Pred. No. 1e-4;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATTAATGAATATGAATGTTGATGCTTTACGAATCAACTTAATATGCTAAT 72
Db 740 AATTAATCAAAATGAATATGAATTAATGATGCAACCTTCTA---CTTGTATCCAAAT 786
QY 73 TGTATCCAGATATCCACTAGCAAAAGATCACAATGACTATGCGAAACAGAACTAT 132
Db 797 GATTTACAGATATACCTTTTGGAAATGAGCAACAAATCGGTACAAAATATGATTAAT 856
QY 133 AAGAAATGCTAAATATGTGTGATTTCAATATACATTAATTTGTGATATATAGACGAT 192
Db 857 AAGATATATTTAAATATGTCTCGGGAAGTATGAAATACCTCGTTCA----- 907
QY 193 TCTAGCCCTGAAGTCTGTATAGTATACGAGATGCTTTTAAACGGGTATTAACAGTGA 252
Db 908 -----CCTGAATTAATCTGTGGCCCTTCAAGGGAAGATGCAATTTTATATGAA 961
QY 253 GGGACTAATCTTGAATTTATGGGGTCCCTTTGGCAAGTCAATTTGGAATTAATAGT 312
Db 962 GGTAAATTAATCAAGTTTATAGGGGTCCCATTTGTTGGCGGATATGATGATCTTAACT 1021
QY 313 AGGCTAATAGTATTTTATGGGCGGCTGA-----TCCATTTGAAGCACTTATGCTT 366
Db 1022 CAATTAATGATATATCTGTGGCCCTTCAAGGGAAGATGCAATTTTATATGAA 1081
QY 367 CTGTGTAAGAGCTTATTAAGAAATATATGATCAAGCTATAGAGAAATGCTTTAGA 426
Db 1082 CAAGTAAAGAACTCATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTTCG 1141
QY 427 GAGCTAAGATTTTACAGGGAATTAATGACTATATCAAACTGACATGCAAGAGCTGA 486
Db 1142 GAATTAAGAAATTAAGTATATTAATCAATTTATATCTAATCTGCTTGAAGAAATGGA 1201
QY 487 GTTAACAAAGATGATGACAAATCGAGGGCACTAGT---AAGGAGTATGCAATTTGAT 543
Db 1202 GAAATTCCAAAATGTTCAAGAGCTTACGAGATGTCGAAATGATTTGAAATCTGGAT 1261
QY 544 AACTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTATTTGTA 603
Db 1262 AGTTATATTTACGCAATATATGCGCATCTTTTGAAGTACAAATTTTGAAGTACCAATTCCT 1321
QY 604 CCAATATATGCAAGAGCGGGAATTTGCAATTTATTTTAAAGATGCTGATATTTT 663
Db 1322 ACTGTAATATGCAATGAGCAAGCAACCTTCATTTACTGTTATTAAGAGCGGTCATTTT 1381
QY 664 GGAGCAGTGGCAATTTAGGTGATGATGAATTCGTGATATTAATATCAAGCTACAGGA 723
Db 1382 GGAGAAATATGGGATGATGATCAACACTAATTAATTAATATGATGATGCTCAAAATGAAA 1441

```



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PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 2022
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2022)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-2A
US-11-108-389-13

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Query Match 11.4%; Score 234; DB 7; Length 2022;

Best Local Similarity 56.4%; Pred. No. 1.8e-44; Mismatches 385; Indels 27; Gaps 4;

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13 AAAAAATGAATGAATGAATGTTGAGCTTTAGCAATCACTTAATATGCTTAAT
10 AATATCAAAATGAATGAATGATATGATGCGACCTTCTA---CTTCTGATCAAT
66
73 TGTATTCAGAGTATCCACTGACGAAAGATCCAAATGACTATGCAACAGCACTAT
67 GATTCTAACAGATCCCTTTTGGCAATGACCAAAATGCGCTACAAATATGATTAAT
126
133 AAGAAATGCTAAATATGATGATCAAAATCAAAATTAATGCTATTAAGACCTAT
127 AAGATATTAATTAATAATGTCGCGGAAATGCTAGTAATACCTGATTC-----
177
193 TCTAGCCCTGAGCTGCTTAATGATGATGATGCTGTTTAAAGGCTATTAACAGTGA
178 -----CTGAGACTGTTGTTAGCGGACAAAGATGACACTAAAGCGCAATGATATGTA
231
253 GGAATATATCTTCTGAAATTTAGGGGCTCTTTGGCAAGTCATCTTGAATTAATAGT
232 GGTAAATTTACTATCAGGTTTAGGGGCTCCATTGTTGGCCGATAGTGAATCTTATATCT
291
313 AGCTATATAGTATTTATTTAGGGGCGGCTGA-----TCCATTGAAGCACTATAGTT
351
292 CAATTAATATATCTCTGCGCTTCAGGCGCAAAAGATCAATGGAGATTTTATGAA
351
367 CTGTTGAGAGCTTATTTAAGAAAGATATGATCAGGCTGTAAGAAATGCTCTTGA
426
352 CAAGTAAAGAACTCAATTAATCAAAATGACAGAAATATGACAGAAATTAAGCGCTTTCG
411
427 GACCTAGAGGTTTACAGGAAATTTATGAGACTATATCAAACTGACGACAGATGCTA
486
412 GAATTAAGAGATTAAGTAAATTAATTAATCAATTAATCTAATGCGCTTGAAGATGAAA
471
487 GTTAACAGATATGATCAATCGAGGCACTAGT---AACGAGTATGCAATTTGTTGAT
543
472 GAAATTCCAATGTTTCAGAGCTTACGAGATGTCGAAATGATTTGAAATTCCTGAT
531
544 AACCTTTTCAAAAGATATGCAAAATTTCAAGAAAGAAATTTGAATTTTATGTTA
603
532 AGTTTATTTAGCAATATGATGCTCTTTTGAAGTCAAAATTTGAAGTCAATCTT
591
604 CAGATATATGACAAAGCGGAAATTTGATTTAATTTATTAAGAGATGCTGATTTAT
663
592 AAGATATATACAGGCAACCTTCAATTTACTGTTATTAAGAGCGCTTCAATTTT
651
664 GAGACATAGTGCATTAAGTATGATGAATTTGATATTAATTTATCAACTACAGGA
723
652 GGAAGAAATGAGGATGCTCAACCACTATTAATTAATTAATGATGCTCAAAATGAAA
711

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724 CTGATTAAGAAATTAAGATCATTTGATTAACATTTCTAATACCAAGGTTTAATCAATTT
783
712 CTTAATCAAGAAATTTCTGATCACTGTGTAAGGATGATAAATGTTTAGCAAAATTA
771
784 AATGCTCAAAATGCTCAAGATTTGGGTGACCTTTAATAGTTTCTGATACAGATGACATTA
843
772 AAAGCAGAGCGGTAAACAATGAGTGTGACTATTAACCAATTCGTAGAGAAATGACCTG
831
844 ACAGTATTAATGATCTGCAATATTTATTTCAAACTATGATCCAGTATGCTATTTAGCA
903
832 ACGGTTTAAATGATGTTGTTGATTTATTCCTCAATTTATACACAGCACTGACCTCAATGAA
891
904 GTAAAAACGAAATTTGACTAGGAAATTTATTAACAGATCCAGTAGG 947
892 ACGAAACCACTAAACAGGAAATGATATATACAGATCCAGTGGG 935

```

RESULT 9

US-11-058-727-3

Sequence 3, Application US/11058727

Publication No. US20050261483A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Ronald D. Flannagan

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: Albert L. Lu

APPLICANT: Billy Fred McCutchen

APPLICANT: James K. Presnail

APPLICANT: James F. H. Wong

APPLICANT: Cao-Guo Yu

TITLE OR INVENTION: Genes Encoding Proteins With Pesticidal

FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: US/11/058,727

CURRENT FILING DATE: 2005-02-15

PRIOR APPLICATION NUMBER: 60/391,786

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787

PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 3633

TYPE: DNA

ORGANISM: Bacillus thuringiensis

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(3633)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (0)...(0)

OTHER INFORMATION: CRY1218-2

US-11-058-727-3

Query Match 11.4%; Score 234; DB 7; Length 3633;

Best Local Similarity 56.4%; Pred. No. 2.2e-44; Mismatches 385; Indels 27; Gaps 4;

```

13 AAAAAATGAATGAATGAATGTTGAGCTTTAGCAATCACTTAATATGCTTAAT
72
10 AATATCAAAATGAATGAATGATATGATGCGACCTTCTA---CTTCTGATCAAT
66
73 TGTATTCAGAGTATCCACTGACGAAAGATCCAAATGACTATGCGAAACAGCACTAT
132
67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAAGATGCGCTACAAATATGATTAAT
126
133 AAGAAATGCTAAATATATGATGATTTCAATTAACAAATTTATGCTGATATTAAGACGAT
192
127 AAGATATTAATTAATAATGTCGCGGAAATGCTAGTAATACCTGATTC-----
177

```

QY 193 TCTAGCCCTGAGCTGCTTAAAGTACGAGATGCTGTTTAAACGGGTATTAACAGTGA 252
Db 178 -----CCTGAAGTACTTGTGTACCGACAAGATGCGATTAAGGCCCAATGTATATGA 231
QY 253 GGGACTATCTTTCGAATTTAGGGGGTCCCTTTGCGAAGTCAATCATTTGGAAATTAATAG 312
Db 232 GGTAAATTTCTATAGGTTTGGGGTCCCTTTGTTGGCCGATGTAGTCTTTTACT 291
QY 313 AGGCTAATAGTATTTTATGCGAGGGCCCTGA-----TCCATTTGAAGCACTTATGTT 366
Db 292 CAACCTATTGATATTCGTGGCCCTTCAGGGCAAAAAGTCAATGGGAGATTTTATGAA 351
QY 367 CTTGTGAAAGCTTATTAAGAAAAGTATGATCAGCGTGTAAAGAAAATGCTCTTAAG 426
Db 352 CAAGTGAAGACTCAATTAATCAAAAAATGAGAAATGCAAGAAATTAAGCGCTTTGG 411
QY 427 GAGCTGAAGGTTTACAGGGAATTAAGACCTATATCAACTGACCTGCAAGCATGGCTA 486
Db 412 GAATTAAGAGATTAAGTAAATTAATTAACCAATTAATCTAACCTGCTTGAAGATGAAA 471
QY 487 GTTAACAAGATGATGACATCGAGGGGCACTAGT---AACGAGTATGCAATTTGTTGAT 543
Db 472 GAAATTCGAATGCTTCAGAGAGCTTAAGAGATGCGAAATGATTTGAAATCCTGGAT 531
QY 544 AACTTTTGAAAAGATATGCTCAAAATTCAGAGAAAAGAACTTTGAATTTTATGTTA 603
Db 532 AGTTTATTTACGCAATATACATGCTCTTTTCAAGTACAAATTTGAAGTACCATTCCT 591
QY 604 CCAATTTATGCAACAGCCGGAATTTGCAATTTTAAATTTTAAAGATGCTATTTT 663
Db 592 ACGATATATACAGAGCAAGCACTTCATTTATGTTTAAAGACGCTTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTGTATGTAATTCGTATTAATTAATTCAGACTACAGGA 723
Db 652 GGAAGAAATGGGAGTGTCTACACACATTAATTAATTAATGATGTCAAATGAAA 711
QY 724 CTGATTAAGAAATTAAGATCAATTTATTAATCAATTTCAATACAGGGTTAAATCAATT 783
Db 712 CTTACTGCAAGATATTTCTGATCTGTATTAAGTGTATGAAACTGGTTTAAAGAAATTA 771
QY 784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTAAATAGAGTTTGTACAGATATGACATTA 843
Db 772 AAAGGACAGGCGCTTAACATGAGTGTGATTAATCAATTCGTAGAGAAATGACAGCTG 831
QY 844 ACAGTATTAATTCGCAATATTAATTTCCAACTATGATCCAGTATGATCCATTAAGA 903
Db 832 ACGGTTTATGATTTGTGTGATTAATTCGCAATTAATGACACAGCAAGTACCAATGAA 891
QY 904 GTAAAAACGGAATTAAGTGAAGGAAATTTATACAGATCCAGTACG 947
Db 892 ACGAAAGCACACTTAACAGGGAATTAATTAACAGATCCAGTACG 935

RESULT 10
US-11-108-389-3
; Sequence 3, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McOutchen
; APPLICANT: James K. Presnall
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CRY1218-2
US-11-108-389-3

Query Match 11.4%; Score 234; DB 7; Length 3633;
Best local similarity 56.4%; Pred. No. 2,2e-44;
Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAATGTTGATGCTTTACGATCACTTAATATGCTTAAT 72
Db 10 AATAATCAAAAGAAATATCAATTAATTAATGAGACCTTCTA---CTTCTGATCCAA 66
QY 73 TGTATCCAAAGATCCATACGAAAGATCCAAAGATGATGCGAAGCAAGCTAT 132
Db 67 GATTTCAAGATATCCCTTTTGCAGATGAGCCAAAGATGCGTCAAAATATGATTA 126
QY 133 AAAGATGCTTAATATGATGATTCAAATATACAAATTAATTTGATATTAAGCAGTAT 192
Db 127 AAAGATTAATTAATAATGCTCGGGAAATGCTAATGAAATCCGTGTTCA----- 177
QY 193 TCTAGCCCTGAGCGCTTAAAGTATGAGAGATGCTGTTTAAACGGGTATTAACAGTGA 252
Db 178 -----CCTGAAGTACTTGTGTACCGACAAGATGCGATTAAGGCCCAATGTATATGA 231
QY 253 GGGACTATCTTTCGAATTTAGGGGGTCCCTTTGCGAAGTCAATCATTTGGAAATTAATAG 312
Db 232 GGTAAATTTCTATAGGTTTGGGGTCCCTTTGTTGGCCGATGTAGTCTTTTACT 291
QY 313 AGGCTAATAGTATTTTATGCGAGGGCCCTGA-----TCCATTTGAAGCACTTATGTT 366
Db 292 CAACCTATTGATATTCGTGGCCCTTCAGGGCAAAAAGTCAATGGGAGATTTTATGAA 351
QY 367 CTTGTGAAAGCTTATTAAGAAAAGTATGATCAGCGTGTAAAGAAAATGCTCTTAAG 426
Db 352 CAAGTGAAGACTCAATTAATCAAAAAATGAGAAATGCAAGAAATTAAGCGCTTTGG 411
QY 427 GAGCTGAAGGTTTACAGGGAATTAAGACCTATATCAACTGACCTGCAAGCATGGCTA 486
Db 412 GAATTAAGAGATTAAGTAAATTAATTAACCAATTAATCTAACCTGCTTGAAGATGAAA 471
QY 487 GTTAACAAGATGATGACATCGAGGGGCACTAGT---AACGAGTATGCAATTTGTTGAT 543
Db 472 GAAATTCGAATGCTTCAGAGAGCTTAAGAGATGCGAAATGATTTGAAATCCTGGAT 531
QY 544 AACTTTTGAAAAGATATGCTCAAAATTCAGAGAAAAGAACTTTGAATTTTATGTTA 603
Db 532 AGTTTATTTACGCAATATACATGCTCTTTTCAAGTACAAATTTGAAGTACCATTCCT 591
QY 604 CCAATTTATGCAACAGCCGGAATTTGCAATTTTAAATTTTAAAGATGCTATTTT 663
Db 592 ACGATATATACAGAGCAAGCACTTCATTTATGTTTAAAGACGCTTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTGTATGTAATTCGTATTAATTAATTCAGACTACAGGA 723
Db 652 GGAAGAAATGGGAGTGTCTACACACATTAATTAATTAATGATGTCAAATGAAA 711
QY 724 CTGATTAAGAAATTAAGATCAATTTGATTAATCACTTATTAACAGGGTTTAAATCAATT 783

Db 712 CTACTAGCAGAAATATCTGATCACTGTGTAAAGTGATGAAACGTGGTTAGCAAAATTA 771
Qy 784 AATCGCTCAAAATCTCAAGTTGGTGAGCTTTAAATAGCTTTGTACAGATAGACTTA 843
Db 772 AAAGGACGAGCGCTAAACAAATGGTTCGACTATACCAATTCGGTAGAGAAAGACACTG 831
Qy 844 ACAGTATGATCTCCCAATATATTTCCAACTAGATCACTAGTAGTATCCATTAGCA 903
Db 832 ACGGTTTAGATTTGTGTGATTTATTCCTCAATTTAGACACGACGATCCCAATGGAA 891
Qy 904 GTAAACCGGAATGACTAGGAAGTTTATACAGATCCAGTAGG 947
Db 892 ACGAAAGCAACAATAACAGGAAGATATATACAGATCCACTGGG 935

RESULT 11

US-11-058-727-18
; Sequence 18, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FaSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6613
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic Ctry1218-2
US-11-058-727-18

Query Match 11.4%; Score 234; DB 7; Length 6613;

Best Local Similarity 56.4%; Pred. No.2,6e-44;
Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

Qy 13 AAAAAATAAATGAATATGATGATGCTTTACGAATCACTTAATATGCTTAAT 72
Db 1263 AATAATCAAAATGAATATGATGATGATGATGATGATGATGATGATGATGAT 1319
Qy 73 TGTATCAAGATGATCAGTACGAAAGATCCCAATGATGATGATGATGATGATGAT 1332
Db 1320 GATTCTAACGATACCTTTTGGATGATGATGATGATGATGATGATGATGATGAT 1379
Qy 133 AAGAAATGCTAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 192
Db 1380 AAGATATATTTAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1430
Qy 193 TCTAGCCCTGAAGCTCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 252
Db 1431 -----CTGAAAGTACTTGTATGCGGACAAAGATGATGATGATGATGATGAT 1484

Qy 253 GGGACTATACCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCAATTTGGAATTAAGT 312
Db 1485 GGTAAATCTATCAAGTTTAAAGGTCCTTATGTTGTTGGGCGGATGATGATGATGAT 1544
Qy 313 AGGCTAATAGATTTTATTTAGGCGAGGCGCTGA-----TGCATTTAGACATTAAGT 366
Db 1545 CAACATTATGATATCTGTGGCTTCGAGGCAAAAGATCAATGAGATTTTATAGGAA 1604
Qy 367 CTTGTTAAAGAGCTTTTAAAGAAAGATTAATGATCAGGTGTAAAGAAATGCTTTAG 426
Db 1605 CAAGTAAAGAACTCAATTAATCAAAATTAATGATGATGATGATGATGATGATGAT 1664
Qy 427 GAGCTAAGAGTTTACAGGAATTAATGATGATGATGATGATGATGATGATGATGAT 486
Db 1665 GAATTGAAGATTTAGGTAATATTAATCAATTAATATCTAATCTGCTGTAAGATGGA 1724
Qy 487 GTTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
Db 1725 GAAATCCAAATGCTTCAAGAGCTTACGATGATGATGATGATGATGATGATGAT 1784
Qy 544 AACTTTTGAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
Db 1785 AGTTATTTAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1844
Qy 604 CCAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
Db 1845 ACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1904
Qy 664 GGAGCAGCTGCAATTTAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
Db 1905 GGAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1964
Qy 724 CTGATTAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
Db 1965 CTACTGCAAAATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2024
Qy 784 AATCGCTCAAAATCTCAAGTTGGTGAGCTTTAAATAGCTTTGTACAGATAGACTTA 843
Db 2025 AAAGGACGAGCGCTAAACAAATGGTTCGACTATACCAATTCGGTAGAGAAAGAC 2084
Qy 844 ACAGTATGATCTCGCAATATTTATTTCCAACTAGATGATGATGATGATGATGATGAT 903
Db 2085 ACGGTTTAGATTTGTGTGATTTATTCCTCAATTTAGACACGACGATCCCAATGGA 2144
Qy 904 GTAAACCGGAATGACTAGGAAGTTTATACAGATCCAGTAGG 947
Db 2145 ACGAAAGCAACAATAACAGGAAGATATATACAGATCCACTGGG 2188

RESULT 12

US-11-108-389-18
; Sequence 18, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 6613
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic Cyl1218-2
US-11-108-389-18

Query Match 11.4%; Score 234; DB 7; Length 6613;
Best Local Similarity 56.4%; Pred. No. 2.6e-44;
Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

13 AAAAAAATGAAATGAAATGTTGATGCTTTCGATCACTTAATGCTAT 72
1263 AATTAATCAAAATGAAATGAAATGATGACACCTTCTA--CTTCTGATCAAT 1319
73 TGTATCCAGGATCTCCTAGCAAAAGATCCAAATGACTATGCGAAACGAATCTAT 132
1320 GATTCGAAGATACCTTTTGCGATGACCAACAAATGCCCTACAAATATGATTTAT 1379
133 AAGAAATGCTAAATATGTTGATCAATACAAATTTATTTGATATTAAGCAGTAT 192
1380 AAGATTTATTTAAAAATGCTCGCGGAAATGCTAGTAATACCTGGTTCA----- 1430
193 TCTAGCCCTGAAGCTCTTAAAGTATGACAGATGCTGTTTAAACGGTATTTAACATGTA 252
1431 -----CTGAAGTACTTTGTTAGCGACAAAGATGACGTAAAGCCCAATGATATAGTA 1484
253 GGGACTATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAATAGT 312
1485 GGTAAATTTCTATCAGGTTTAAAGGATCCCATTTGTTGGCCGATATGATGCTTTTACT 1544
313 AAGCTAATAGTATTTTATGAGGAGGAGGCTGA-----TCCATTTGAAGCACTTATGTT 366
1545 CAATTAATGATATCTGTGCGCTTCAAGGCAAAAGATCAATGAGAGATTTTATATGAA 1604
367 CTGTTGAAGAGCTTTTAAAGAAATATATGATCAAGGATGTAAGAAATGCTCTTAA 426
1605 CAAGTGAAGAACTCAATTAATCAAAATTAATGCAATATGCAAGAAATTAAGGCTTTG 1664
427 GAGCTGAAGGTTTACAGGAAATATGAGCTATATCAACTGATGCAAGCATGCTTA 486
1665 GATTTGAAGGATTTAGTATATATATACATTTATCTAATCTGCGCTTGAAAGATGAAA 1724
487 GTTAACAAATGATGACAAATCGAGGCACTAGT--AAAGCATATGCAATTTGAT 543
1725 GAAATCCAAATGCTTCAAGAGCTTACGAGATGTCGAAATGATTTGAAATCCGTGAT 1784
544 AACTTTTGGAAAGAAATATGCAAAATTCAGAGAAAGAACTTGAATTTTATGTTA 603
1785 AGTTTATTTACGCAATATACATGCTTTTTCAGATGACAAATTTTAAAGCATTCCTT 1844
604 CCAGTATATGACAAAGCCGCAATTTGCAATTTTATTTTATTAAGAGATGCTGATTTT 663
1845 AAGATTTATACACAGGACCAACCTTCAATTTCTGTTATTAAGAACGCTTCAATTTT 1904
664 GGAGCACTGCGCAATTAAGTATGATGAATTCGTATTAATTAATCAAGACTACAGAA 723
1905 GGAGAAATGAGGAGATGCTTCAACCACTAATTAATTAATATGATGCTCAATGA 1964
724 CTGATTAAGAAATTAATGATCTTTTATTAACATTTCTATTAACAGGTTTAAATCAATTT 783
1965 CTTAATGCAAGATATTTCTATATCTGTTGTAAGATGATGAATCTGTTTAAAGAAATTA 2024
784 AATGCTCAATGCTCAAGATTTGGTGAAGCTTAAATAGGTTTGTACAGATATGACATTA 843
2025 AAGGCAAGAGGCTTAAACAAATGGATGACATATTAACCAATTCGTTAGAAATGACACTG 2084

844 AAGATTTAGATCTGCAATATTTTCCAACTATGATCCACGTAGTATCCATTAGCA 903
2085 ACGGTTTAAAGATGTTGTTGATTTATTCCTCAATTTATGACACAGCACTGACCAATGAA 2144
904 GTAAAAAGCAATGACTAGGAAATTTATACAGATCCAGTAGG 947
2145 ACGAAAGCAACATTAACAAAGGAATATATACGATCCACTGG 2188

RESULT 13
US-11-058-727-7
Sequence 7; Application US/11058727
Publication No. US20050261483A1

GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7

LENGTH: 2022
TYPE: DNA
ORGANISM: Bacillus thuringiensis (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2022)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: NSR.N1218-1
US-11-058-727-7

Query Match 11.0%; Score 225.2; DB 7; Length 2022;
Best Local Similarity 55.9%; Pred. No. 1.8e-42;
Matches 534; Conservative 0; Mismatches 383; Indels 39; Gaps 4;

13 AAAAAAATGAAATGAAATGTTGATGCTTTCGATCACTTAATGCTAT 72
10 AATTAATCAAAATGAAATGAAATGATGACACCTTCTA--CTTCTGATCAAT 66
73 TGTATCCAGGATCTCCTAGCAAAAGATCCAAATGACTATGCGAAACGAATCTAT 132
67 GATTCGAAGATACCTTTTGCGATGACCAACAAATAGCCCTCAAAATATGATTTAT 126
133 AAGAAATGCTAAATATGTTGATTCAAATTAACAAATTTATTTGATATTAAGCAGTAT 192
127 AAGATTTATTTAAAAATGCTCGGAAATGCTAGTAATACCTGGTTCA----- 177
193 TCTAGCCCTGAAGCTCTTAAAGTATGACAGATGCTGTTTAAACGGTATTTAACAGTGA 252
178 -----CTGAAGTACTTTGTTAGCGACAAAGATGACGTTAAGCCCAATTTGATATAGTA 231
253 GGGACTATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCAATTTGGAATTAATAGT 312
232 GGTAAATTTCTATCAGGTTTAAAGGATCCCATTTGTTGGCCGATATGATGCTTTTACT 291

```

QY      313  AGGCTAAATAGGATTTTAAATGGGACGGGCGCTGA-----TCGATTTGAAGCACTTAAGTGT 366
Dp      292  CAACCTTATGATATATCTGTGGCCTTCAGGGGAAAAGATCAATGGAAATTTTATGGAA 351
QY      367  CTGTGTGAAGACCTTATTAAGAAAAGTATAGATCAGCGTGTAAAGAAAATGCTCTTGA 426
Dp      352  CAAGTGAGAAGAACTCTTATATCAAAAATATGCAAGATATGCAAGAAATAAAGGCTTTGC 411
QY      427  GAGCTAGAAGGTTTACAGGGAATTATGACATATATCAAACTAAGACTGCAGACATGGCTA 486
Dp      412  GAAATTAGAAGGATTTAGTAAATTAATTAACCAATTATATCTAACTCGCGCTGGAAGAATGGAA 471
QY      487  GTTAAACAAGAAATGACAAATGGAAGGGGCACTAGT-----AAGCAGTAT 531
Dp      472  GAAAAATCCAAATGGTTCAAGAAATGGTTCGCGGCGCTTACGAGATGTGCGAAATTCATTT 531
QY      532  GCAATTTGTGATTAACCTTTTTCGAAAAGAAATATGSCAAAATTCAGAGAAAAGAACTTGA 591
Dp      532  GAAATCCCTGGAATAGTTTATTTAAGCAATATATGCCATCTTTAAGATGACAAATTTGAA 592
QY      592  ATTTTATTTGTTACCAAGTATATGSCAACAGCCGCGAATTTGCATTTAAATTTTAAAGAT 651
Dp      592  GTACCACTTCCTTACGTATATATGCAATGCGACGCAACTTCATTTACGTATATTAAGAAC 651
QY      652  GCTGATTTATTTTGGACACAGTGGCAATTAAGGTATGATGAATTCGTGATATTTATATC 711
Dp      652  GCGTCAATTTTGGAGAGAAATGGGGATGTCAACAACACTATTTATTAATCTTTTATGAT 711
QY      712  AGACTACAAGACGCTGATTTAGAAATTAATAAGATCATTTATTAACCTTATACAGGGGT 771
Dp      712  CGTCAATAGAACTTATCTGACAGAAATTTCTGATCATCTGTGTAAAGTGATGAAACTGGT 771
QY      772  TTAATATCAATTTAATCGCTCAAAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTCTGACA 831
Dp      772  TTAGCAAAATTTAAAGGACGACGCGCTAAACAATGCGTTGACATTAACCAATTCGTAAGA 831
QY      832  GATATGACATTTAACGATATTAATATCTCGCAATTTTTCGCAACTATGATCAAGTAAAG 891
Dp      832  GAAATGACACATCGGCGGTTTTAATATGTTGTGCAATTAATCCCAATATATGACACACGACG 891
QY      892  TATCCATTAGCAGTAAACGGAATTTGACTAGGGAAGTTTATACAGATCCAGTAGG 947
Dp      892  TATCCCAATGGAACGAAAGCACACTTAACAAGGAAATGATATACAGATCCACTGGG 947

RESULT 14
US-11-058-727-25
/ Sequence 25, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ TITLE OF INVENTION: Activity
/ FILE REFERENCE: 35718/287809
/ CURRENT APPLICATION NUMBER: US/11/058, 727
/ CURRENT FILING DATE: 2005-02-15
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25

```

	LENGTH: 2022	
/	TYPE: DNA	
/	ORGANISM: Bacillus thuringiensis (mutated)	
/	FEATURE:	
/	NAME/KEY: CDS	
/	LOCATION: (1) ... (2022)	
US-11-058-727-25		
Query Match	11.0%; Score 225.2; DB 7; Length 2022;	
Best Local Similarity	55.9%; Pred. No. 1.8e-42;	
Matches 534; Conservative	0; Mismatches 383; Indels 39; Gaps 4	
OY	13 AAAAAATAAATGAAATATGAATAGTGGATCGTTACGAATCACTTAATATGTCTAT	72
DB	10 AAATATCAAATGAAATATGAATATGAATGAGACACTTCCTTCTATTCATAT	66
OY	73 TGTATCCAAAGATATCCACTAGCAAAAAGTCCAACAATGACTATGCGAAACAGAATAT	132
DB	67 GATTCTAACAGATACCCTTTTGCGAATGAGCCAAACAATGGCGTCAAAAATATGTATTAT	126
OY	133 AAAAGATGGCTPAATATATGTGTGATTCAAATAACAAATTTATTTGTGATATTAAGCACGTAT	192
DB	127 AAAAGATTTATTAATAATGTCTGCGGGAATCTAGTGAATACCTCTGTCTCA-----	177
OY	193 TCTAGCCCTGAAGCGCTTTAAGTGTACGAGATGCTGTTTTAACCGGTATTAACATGTA	252
DB	178 -----CCTGAAGATACCTTGTAAGCGCAAGATGCAAGCTTAAGGCCCAATGATATPATGA	231
OY	253 GGGAATATACCTTTCGAATTTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAATTAATTAAGT	312
DB	232 GGTAAATTAATCAATCAGGTTTAGGGGTCCCATTGTTGTGGCCGATAGTGCCTTTATACT	291
OY	313 AGGCTAATAGATATTTATATGGGACAGGGCCCTGA-----TCAATTTGAAGCACTTATGTT	366
DB	292 CAACATTAATGATATCTGTGGCCTTCAGGGGAAAAGATGCAATGGGAATTTTATNGAA	351
OY	367 CTGTGTGAAGCTTATTAAGAAAAAGTATAGTACGCGTGTATAGAGAAAAATGCTCTTAGA	426
DB	352 CAAGTAGAAGAACTCATTAATCAAAAAATACAGAAATATGCAAGGAATTAACCGCTTTGCG	411
OY	427 GAGCTAGAAGGTTTACAGGAATTAATGAGATATATCAATCAACTGACCTGCAAGCTAGGCTA	486
DB	412 GAATTTAGAGATTTAGTATTAATTAACCAATTAATATCTAATCTGCGCTGAGAAATGGGAA	471
OY	487 GTTAAACAAGATGATGACATCGAGGSCACTAGT-----AAAGCAGAT	531
DB	472 GAAATCCAAATGTTGCAAGAAATGTTCCGGGCGCTTAACGAGATGTCGAAATGATATT	531
OY	532 GCATTTGTTGATTAACCTTTTGAAAAAGATATGCCAAATTCAGAGAAAGAACTTTGAA	591
DB	532 GAAATCCGATAGTTTATTTAAGCAATATATGCGATCTTTTAGATGACAAATTTTGGAA	591
OY	592 ATTTTATTTGTACAGATATATGCAACAACCGCGAATTTGCAATTTATTTTATTAAGAT	651
DB	592 GTACCAATCTTACGTATATGCAATGCAAGCAACCTTCATTTACTGTTATTTAAAGAC	651
OY	652 GCTGATTTATTTGGAGCAGATGCGCAATTAAGTGTATGAAATCGTATTAATTAATATC	711
DB	652 GCGTCAATTTTGGAGAGAAATGGGGAATGTCACAACTACATTAATTAATCAATATATGAT	711
OY	712 AGACTCAACAAGCTGATTAAGAAATATTAAGATCATTTGTATPACATTTCTATPACAGAGGT	771
DB	712 CGTCAAAATGAACCTTACGAGAAATATCTGATCACTGTATTAAGTGTATGAACCTGTT	771
OY	772 TTAAATCAATTTAATCGCTCAAAAGCTCAAAATTTGGGGAGCTTTAATAGGTTTGSTACA	831
DB	772 TTAGCAAAATTTAAAGGACGACGAGCTTAACAAATGGGTTGACTATPACAAATTCGTTAGA	831
OY	832 GATATGACATTAACAGATATAGATCTCGCAATATATTTCCAAACTATGATGACAGTAGG	891
DB	832 GAATATGACATCGGCGGTTTATAGATGTTTGTGATTAATTCGCAAAATTAAGACACAGCAGC	891
OY	892 TATCCATTAGACGTAAAAAGCAAAATGACTAGGGAAGTTTATPACAGATCCAGTAGG	947

Db 892 TACCAATGAAACGAAACACAACTAACAGGAAGTATATACAGATCCACTGGG 947

RESULT 15
US-11-058-727-29
Sequence 29, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flanagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F. H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 2022
TYPE: DNA
ORGANISM: Bacillus thuringiensis (mutated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2022)
US-11-058-727-29

Query Match 11.0%; Score 225.2; DB 7; Length 2022;
Best Local Similarity 55.9%; Pred. No. 1.8e-42;
Matches 534; Conservative 0; Mismatches 383; Indels 39; Gaps 4;

Db 412 GAATTGAAAGATATGATATATATATACAAATTAATCTTACTGCGCTTGAAAGATGGAA 471
Qy 487 GTTAAACAAGATGATGACAAATCGAGGCACTAGT-----AACGAGTAT 531
Db 472 GAAATCCAAATGGTTCAAGAAATGGTCCGGGCTTACGAGATGGGAAATGCATTT 531
Qy 532 GCAATGTTGATTAACCTTTTTCGAAAAGAAATATGCCAAAATTCAGAGAAAGAACTTTGAA 591
Db 532 GAAATCCGATAGATTTATTAACGAAATATATGCCATCTTTAGAGTGAACAAATTTTGA 591
Qy 592 ATTTTATGTTACGATATATGCAACAGCGGAAATTCATTTATTTATTAAGAT 651
Db 592 GTACATTCCTTACTGATATATGCAATGGCAACCACTTACTGTTATTAAGAC 651
Qy 652 GCTGATTTATTTTGAGACAGTGGCAATTAAGGTATGATGAAATTCGATTAATATATC 711
Db 652 GCGTCAATTTTGGAGAAAGATGGGATGCTCAACAACACTATTAATTAATATATATGAT 711
Qy 712 AGACTACAAAGACTGATTAAGAAATTAAGATCATTGATTAACATTCATTAACAGGAT 771
Db 712 CGTCAAAATGAAACTTACTCAGAAATATCTGATCACTGATTAAGTATGAACCTGGT 771
Qy 772 TTAATCAATTTAATGCTCAAAATGCTCAAGATTTGGTGAGCTTTAATAGTTGATAC 831
Db 772 TTAGCAAAATTAAGGACAGAGCGCTAACAATGGGTGACTATTAACCAATTCGTTAG 831
Qy 832 GATATGACATTAACAGTATTAATGATCTCGCAATTAATTTCCAAACTATGATCCAGTAG 891
Db 832 GAAATGACACTGGCGTTTATGATGTTGCTTATTCGCAAAATATATGACACAGCAG 891
Qy 892 TATCCATTAGCAGTAAACGGAATTTGACTAGGAAAGTTTATACAGATCCAGTAG 947
Db 892 TACCAATGAAACGAAACGAAACCAACTAACAGGAAGTATATACAGATCCACTGGG 947

Search completed: December 24, 2005, 19:26:23
Job time : 308 secs

Qy 13 AAAAATAAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
Db 10 AATTAATCAAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 66
Qy 73 TGTATCAAGATGATCACTAGCAAAAGATCCAAATGATGATGATGATGATGATGATGAT 132
Db 67 GATTTACAGATACCTTTTGGCAATGAGCCAAATGCGCTACAAATATATGATATAT 126
Qy 133 AAAAATGCGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 192
Db 127 AAAGATTAATTAATAAATGCTGCGGAAATGCTAGTGAATACCTGGTCA----- 177
Qy 193 TCTAGCCCTGAGCTGCTTTAAGTACAGAGATGCTGTTTAAACGGATTAATTAACAGTGA 252
Db 178 -----CTGAGTACTTGTATGCGGACAAAGATGCAAGCTAAGGCCGCAATGATATAGTA 231
Qy 253 GGGACTATATCTTGAATTTAGGGGTCCTTTGGCAAGTCAATCAATTTGGAATTAATAGT 312
Db 232 GGTAAATTAATCAAGTTTAAAGGGTCCCATTTGTTGGGCGATAGTGAATCTTTTACT 291
Qy 313 AGGCTAATAGTATTTTATGCGGAGGCGCTGA-----TCCATTTGAAGCACTATAGT 366
Db 292 CAACCTAATGATATCTGCGCTTCAAGGGAAGAGTCAATGGGAATTTTATAGAA 351
Qy 367 CTGTGAGAGGCTTATTAAGAAAGATATGATCAGCGTGTAAAGAAATGCTTTAGA 426
Db 352 CAAGTAAAGACTCATTAATCAAAAAATGCAAGATATGCAAGAAATTAAGCGCTTTG 411
Qy 427 GAGCTAAGAGTTTACAGGGAATTAAGACTATATCAAACTAGACTGCAAGCATGGCTA 486

QY GGGCATATACCTTGGAAATTTAGGGGGTCCCTTTGGCAACATCATCTTTGGAAATTAATGT 312
 Db |||
 QY 229 GGTCAAGTACTGGGGGCTTTAGGGGTTCCATTGCTGACAGATAGCTAGTTTATATAGT 288
 QY 313 AGGCTAATAGGTATTTTATGAGCAGAGGCT-----GATCCATTTGAAGCATTAATGGTT 366
 Db |||
 QY 289 TTCAATGTCGGTCATTAATGCGCATCAAGTACCGTAGTGTATGGGAATGATTAAGAA 348
 QY 367 CTTGTTGAAGCTTATTTAAGAAAAGTATAGATCAGCGTGTAAAGAAAATGCTCTTGA 426
 Db |||
 QY 349 CAAGTGGAAAGCTTAATTGATCAAAAATAACAGATTCGTAAAGAAAAACGCGTTGCA 408
 QY 427 GAGCTAGAAGGTTTACAGGAAATTTAGACTATATCAAACTAGACTCAAGCATGCGTGA 486
 Db |||
 QY 409 GGACTCAAGATTTAGAGATGCGCTTAGACGTTATCAAGAAATCATCTTAAGAAATGGCTG 468
 QY 487 GTTAAACAAGATGATGACA--ATCGAGGGCACAAGTAAAGCAGATATGCAATGTTGAT 543
 Db |||
 QY 469 GAAATCGTATGATACAAAGAGCTGAAGTGTGTGGTGACCCCAATATATAGCTTTAGAG 528
 QY 544 AACTTTTGGAAAAAGATATGCCCCAAATTCAGGAAAGAAACTTTGAATTTTATGTTA 603
 Db |||
 QY 529 CTTGATTTTGTGCTAAATCCCATCTTTGCAATATCTGACAGAAAGTACCATTTA 588
 QY 604 CCAGTATATGCAACAAGCCGCGAATTTGCAATTTAATTTATTAAGAGTGTGATTAATTT 663
 Db |||
 QY 589 TCAGTGTATGCAACAGACAGCAATTTACATTGCTGATTTATTAAGAGATGCTTCCATTTT 648
 QY 664 GGAGCACAGTGGCAATTAAGTGATGATGAATTCGTGATTAATTAATATATACACTACAGA 723
 Db |||
 QY 649 GGAGCAGAGTGGGGATTCACACAGAGAAATTTCCATTTTATGATGTCAGGTGACA 708
 QY 724 CTGATTAAGAAATTAAGATCATTTGTTAATCATCTTAATCCAGGTTTAATCAATTT 783
 Db |||
 QY 709 CGTACCGCCCAATATCTGATTTATGTGTAAGGTGTAATACACTGGCTTGATTAATTA 768
 QY 784 AATGCTCAAAATGCTCAAGATTTGGGTGAGCTTTAATAGGTTCCATACAGATATGACATTA 843
 Db |||
 QY 769 AAAGTACGATATGCTGCAAGTTGGCTGAAGTATCACAATTCGGAAGAAATGACATTA 828
 QY 844 ACAGTATTAGATCTGCAATATTAATTTCCAACTATGATCCACGTAAGTATTCATTAAGA 903
 Db |||
 QY 829 CTGGTATTAGATTGTAGTCCGTTATTTCCAACTATGACACAGTACGTTATCCATTCGAA 888
 QY 904 GTAAACAAAGCAATGACTAGGGAATTTATCCAGATCCAGTAGGGTTTACTGGGGTATTA 963
 Db |||
 QY 889 ACAACGGCCCACTTACAGGGAGGTATACAGATCCAAATGTATTTAACAGAGAAACA 948
 QY 964 GAAAGTGAGGTAGGA 979
 Db |||
 QY 949 AGTGTGATTTTGTGA 964
 Db |||
 US-10-089-678-3
 RESULT 2
 US-10-089-678-3
 : Sequence 3, Application US/10089678
 : Publication No. US20030017967A1
 : GENERAL INFORMATION:
 : APPLICANT: ASANO, Shintaro
 : TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
 : FILE REFERENCE: Q68821
 : CURRENT APPLICATION NUMBER: US/10/089, 678
 : PRIOR FILING DATE: 2002-05-02
 : PRIOR APPLICATION NUMBER: JP 2000-236140
 : PRIOR FILING DATE: 2000-08-03
 : PRIOR APPLICATION NUMBER: PCT/JP01/06660
 : PRIOR FILING DATE: 2001-08-02
 : NUMBER OF SEQ ID NOS: 3
 : SOFTWARE: PatentIn version 3.1.
 : SEQ ID NO 3
 : LENGTH: 3690

Query Match	11.5%	Score 236	DB 5	Length 3690
Best Local Similarity	55.9%	Pred. No. 2.6e-43		
Matches 546	Conservative 0	Mismatches 400	Indels 30	Gaps 4
Query	13	AAAAATAAATGAATATGTAATGTTGGATGCTTTAGAAATCAACTGAATATGCTTAAT	72	
Ds	196	AATATATCAAAATGAAATGAAATCTAGAGCTTCACTACTA---CTTCTGATTCGAT	252	
Qy	73	TGTATCCAAAGTATCCACTAGCAAAAGATCCAAATGACTATGCAAAACCAACATAT	132	
Ds	253	AATTCCTGTGATACCTCTTTAGCAAAAGATCAACACACATTTACAAAAACATGACAT	312	
Qy	133	AAAGATGCGCTAAATATGTGTGATTCAAATACAAATTTATGTTGATATAGACCGTAT	192	
Ds	313	AAAGATATATCTGAGAAATGCTGAG-----GGAGGAATCTGAAATTA	354	
Qy	193	TCATGACCTTGAAGTGTCTTAAGTACAGATGCTGTTTAAACGGTATTTAAGAGTA	252	
Ds	355	TTTGGAAATCCGGAGAGGTTTATTAAGTTCATCTACGGTTCAACTGGAATGTCATGTT	414	
Qy	253	GGGACTATACCTTTGCAATTTAGGGGCTCCCTTTGGCAAGTCAATCATTTGGAATATAGT	312	
Ds	415	GGTAAAGTACTGGGGGCTTTTAGGGGTTCCATTTCTGACAGATGCTAGTTTATATAGT	474	
Qy	313	AGGCTAATAGGATTTTATGAGGACAGGCGCT-----GATCCATTTGAAGCATTAAGGTT	366	
Ds	475	TTTATGTCGGTCAATTTATGCGCATCAAGTACCGTGAAGTGTATGGAAATGATTATGAA	534	
Qy	367	CTTGTGTAAGAGCTTATTAAGAAAGATATAGATCAGGCTGTAAAGAAATAGCTCTTGA	426	
Ds	535	CAAGTGAAGATCTAATTTGATCAAAAATTAACAGATTTCTGTAAAGAAACAGCGCTTGA	594	
Qy	427	GAGCTAAGAGTTTACAGGGAATTAATAGACTATATCAAACTAGACTGCAAGATGGCTA	486	
Ds	595	GGACTTACAGGATTTAGAGATGCGTTAGACGTATATACGAATCATCTTAAAGATTTGGCTG	654	
Qy	487	GTTAACAAGATATGAC---ATCGAGGGCACAAGTAAACGATATGCAATTTGGAT	543	
Ds	655	GAAATATGATATGATACAAAGAGTAAAGTGTGGTGAACCAATATATAGCTTTAGAG	714	
Qy	544	AACCTTTTCGAAAAGATATGCCAAAATTCAGAAAGAAACCTTGAATTTATGTTA	603	
Ds	715	CTTGAATTTTGTGCTAAATCCCATCTTTTGCAATCTGACAGAAAGTACCATTTTA	774	
Qy	604	CCAGTATATGACAAAGCGGCAATTTGCAATTTATTTATTAAGATAGCATTAATTTT	663	
Ds	775	TCAGTGTATGACACAGAGCAATTTACATTTGCTATTTATTTACAGATGCTTCCATTTT	834	
Qy	664	GGAGCACAGTGGCAATTAAGTATGATAGTAAATTCGATATTAATTTATTCAGACTAACAGA	723	
Ds	835	GGAGCACAGTGGGATTTCAACACAGAGAAATTTCCACATTTATATGATTCGACAGTACA	894	
Qy	724	CTGATTAAGAAATTAAGATCATTTGATTAACATTTCTATTAACAGGGTTTAAATCAATTT	783	
Ds	895	CGTACCCGCCCAATCTCGGATTTATGTGTAAAGGTGATTAACATCGGCTTGTGATTAATTA	954	
Qy	784	AATGCTCAATGCTCAAGATTTGGGTAGAGCTTTAATAGTTTGGTACAGATATGACATTA	843	
Ds	955	AAAGTACGAATGCTGCAAGTTGCTGAAGATATCAAAATTTCCAGAGGAATGACATTTA	1014	
Qy	844	ACAGTATTAAGATCTCGCAATTTATTTCCAAATCATATGATCCACGTAGATTCATTAGCA	903	
Ds	1015	CTGTATTTAGATTTTAGTAGGCTTATTTCCAAACTATGACACAGTACGTATCCATTCGAA	1074	
Qy	904	GTAAAAACGGAATGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGATATTA	963	
Ds	1075	ACAAAGGCGCAACTTACACGGGAAGTGTATACAGATCCAAATATGATTTTAAACAGAAACA	1134	
Qy	964	GAAATGAGAGTACGA	979	

Db 1135 AGTGTGATTTTGTGA 1150

RESULT 3
US-10-032-717-5
Sequence 5, Application US/10032717
Publication No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2003
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2001)
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1
US-10-032-717-5

Query Match 11.5%; Score 235.6; DB 5; Length 2003;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

Qy 13 AAAAAATGAATGATGAAATGTTGATGCTTACGAATCACTTAATGTCTAAT 72
Db 10 AATATCAATGAATGAAATGAAATGATGACACCTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATCAAGATGATCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db 67 GATTTACAGATACCTTTTGGCAATGACCAACAATGCGCTACAAATATGATAT 126
Qy 133 AAGAAATGCTAAATATGTGTGATTCAAATACAAATTAATGATATAGCACTAT 192
Db 127 AAGATTAATTAATAATGTCTGGGGAATGCTAGTGAATACCTGTGCA----- 177
Qy 193 TCTAGCCCTGAGCTGCTTAAGTATGAGATGCTGTTTAAACGGTATTAACAGTGA 252
Db 178 -----CTGAAATGACTGTTAGCGGCAAGATGCAAGCCGCAATTTGATATAGTA 231
Qy 253 GGGACTATCTTTCGAATTTAGGGGTCCTTGGCAAGTCAATCTTGAATTAATAGT 312
Db 232 GGTAAATTAATCAAGTTTAGGGGTCCTTGTGGCCGATGATGATCTTTATCT 291
Qy 313 AGGCTAATAGTATTTTATGGGCAAGGCTGA-----TCCATTTGAAGCACTTAATGTT 366
Db 292 CAAGTATTAATTTCTGTGGCTTCAGGGGAAAGATGCAATGGGAAATTTTATGGA 351
Qy 367 CTGTGTAAGAGCTTATTAAGAAAGATATGATCAGCTGTAAAGAAAATGCTTTAGA 426
Db 352 CAAGTAAAGATCTTAATTAATCAAAAATAGCAAAATATCAAGATTAAGCGCTTCG 411
Qy 427 GAGCTGAAGGTTTACAGGAATTTATGAGCTATATCAATCACTGACGCAAGATGCTA 486
Db 412 GAATTTGAAGGATTTAGTATTAATTAATCAATTAATTAATCTGCGCTTGAAGAAATGGA 471
Qy 487 GTTAACAAAGATATGACAAATCGAGGCACTAGT---AAGCAATATGCAATTTGTTAT 543

Db 472 GAAATTCGAATGCTTCAGAGCTTACGAGATGTGCAATGATTTGAATCCGGAT 531
Qy 544 AACTTTTCGAAAAGATATATGCAAAATTCAGAAAAGAACTTTGAATTTTATGTTA 603
Db 532 AGTTTATTTACGAATATATGCAATCTTTTATGATGCAAAATTTTGAAGATCACTTC 591
Qy 604 CAGATATATGCAAGAGCGGAAATTTGCAATTTAATTTTATTAAGATGCTGATTTAT 663
Db 592 ACTGATATATCAATGAGCAACCTTCATTTACTGTTATTAAGAGCGGTCATATTTT 651
Qy 664 GAGCAAGTGGCAATTAAGTATGATGAATTCGTATATTAATATACACTACAGCA 723
Db 652 GGAAGAAATGGGATGCTCAACAACCTACTAATTAATTAATTAATGATGCTCAATGAAA 711
Qy 724 CTGATTAAGATATTAAGATATGATTAATTAATTAATTAATTAATTAATTAATTAAT 783
Db 712 CTATCTGCAAAATTTCTGATCTGTTAAGTGTATGAATCTGTTTATGCAAAATTA 771
Qy 784 AATGCTCAAAATGCTCAAGATGCTGAGCTTTAATAGTTTGTACAGATATGACATTA 843
Db 772 AAGGACAGAGCGCTAAACAAATGAGTTGACTATTAACCAATTCGTAGAGAAATGAC 831
Qy 844 ACGATATGATCTCGCAATATTTTCCAACTATGATCAAGTATGATCACTTATGCA 903
Db 832 GCGGTTTATGATGTTGATCAATTTCCAAATTAATGACACAGCAAGTACCAATGAAA 891
Qy 904 GTAAAAACGAATGACTAGGAAATTTATACAGATCACTAG 947
Db 892 ACGAAGACACTAACAGGAAATTAATACAGATCACTAG 935

RESULT 4
US-10-414-637-5
Sequence 5, Application US/10414637
Publication No. US20030177528A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20030177528A1e1 Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: US/10/032,717
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2003
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2001)
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1
US-10-414-637-5

Query Match 11.5%; Score 235.6; DB 6; Length 2003;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

Qy 13 AAAAAATGAATGATGAAATGTTGATGCTTACGAATCACTTAATGTCTAAT 72

Db 10 AATAATCAAAATGAAATATGAAATTAATGATGCAACCTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAGAGTATCCACTAGCAAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db 67 GATTCTAACGATATCCTTTTGGCAATGAGCCAAACAAATGCGTACAAAATATGATAT 126
Qy 133 AAAAATGCGTAAATATGATGATTCAAATPACAAATTTATGATGATATAGACGCTAT 192
Db 127 AAAGATATTTAAATATGCTGCGGAAATGCTAGTAATATCCCTGCTTCA----- 177
Qy 193 TCTAGCCCTAGAGCTGCTTAAGTATCGAGATGCTGCTTTTAACGGTATTAACAGTGA 252
Db 178 -----CCTAAGACTTGTATGCGCAAGATGCACTAAGCGCAATGATATATGTA 231
Qy 253 GGGACTATATCTTGAATTTAGGGGCTCCCTTTGGCAATGCAATCATTTGGAATTAATAGT 312
Db 232 GGTAAATATCTATCAGGTTTATGAGGCTCCATTTGTTGGCCGATAGATGATCTTTATCT 291
Qy 313 AGGCTAATAGTATTTTATGAGGCGAGGCTTGA-----TCCATTTGAGCACTTATGCTT 366
Db 292 CAATTAATGATATTTCTGCTGCTTCAAGGGAAGAAAGATGCAATGGCAATTTTATGGA 351
Qy 367 CTGTGTAAGAGCTTATTAAGAAAAGTATGATCAGGCTGTAAGAAAATGCTCTTGA 426
Db 352 CAAGTAAAGAACTCATTTAATCAAAAATATGCAAGATATGCAAGATTAAGCGCTTTCG 411
Qy 427 GAGCTAAGAGTTTACAGGAAATTAATGAGACTATATCAACTAGACTGCAAGCATGGCTA 486
Db 412 GAATTAAGAGATTTAGTAAATATATACCAATTAATATTAATGCGCTGGAAGATGGAA 471
Qy 487 GTTAAACAAGATGATGCAATCGAGGGCACTAGT---AAGCAGATATGCAATTTGAT 543
Db 472 GAAATATCAATGCTGTCAGAGCTTACAGATGTCGAAATGCAATTTGAAATCTGAT 531
Qy 544 AACTTTTTCGAAAAGATATGCCAAATTCAGAGAAAGAACTTGAATTTATTTCTTA 603
Db 532 AGTTTATTTACGCAATTAATGATGCTTTTATGATGCAAAATTTGAAATGCAATTCCTT 591
Qy 604 CCAATATATGCAACAGCGCGAAATTTGCAATTTATTTATTAAGAGATGCTGATTTT 653
Db 592 ACTGTAATATGCAATGCGACCACTTCAATTTACTGTTATTAAGAGCGGCTCAATTTT 651
Qy 664 GGAGCAAGTGGCAATTAAGTATGATGAAATTCGTATTAATTAATCAGACTACAGAGA 723
Db 652 GGAGAAAGATGGGATGCTCAACCACTACTATTAAATATATATGATGCTCAATGAA 711
Qy 724 CTGATTAAGAAATTAAGATCATTTGATTAATCAATTTATTAACAGAGGTTTAAATCAATTT 783
Db 712 CTTAAGTCAAGAAATATCTGATCACTGTATTAAGGATGAACTGGTTTATGCAAAATTA 771
Qy 784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTGTGTAAGATATGACATTA 843
Db 772 AAAGGCAAGAGCGCTTAACATATGCTGATATTAACCAATTCGTAGAGAAATGACCTG 831
Qy 844 ACAGTATTAATCTCGCAATTAATTTTCAAACTATGATCAGATAGTATTCATTAAGCA 903
Db 832 GCGGTTTATATGTTGTTGCTATTTCCAAATTAATGACACAGCAAGTACCCAAATGAA 891
Qy 904 GTTAAACGGAATGACTAGGAAAGTTTATACAGATCAGTAGG 947
Db 892 ACGAAGCAACAACTAACAGGGAAGTATATACAGATCAGTGG 935

RESULT 5
US-10-032-717-15

; Sequence 15, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn

; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
; US-10-032-717-15

Query Match 11.5%; Score 235.6; DB 5; Length 2010;
Best Local Similarity 56.5%; Pred. No. 2.4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

Qy 13 AAAAAATCAAAATGAAATATGAAATTTATGATGCAACCTTCTA---CTTCTGATCCAAAT 72
Db 10 AATAATCAAAATGAAATATGAAATTAATGATGCAACCTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAGAGTATCCACTAGCAAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db 67 GATTCTAACGATATCCTTTTGGCAATGAGCCAAACAAATGCGTACAAAATATGATAT 126
Qy 133 AAAAATGCGTAAATATGATGATTCAAATPACAAATTTATGATGATATAGACGCTAT 192
Db 127 AAAGATATTTAAATATGCTGCGGAAATGCTAGTAATATCCCTGCTTCA----- 177
Qy 193 TCTAGCCCTAGAGCTGCTTAAGTATCGAGATGCTGCTTTTAACGGTATTAACAGTGA 252
Db 178 -----CCTAAGACTTGTATGCGCAAGATGCACTAAGCGCAATGATATATGTA 231
Qy 253 GGGACTATATCTTGAATTTAGGGGCTCCCTTTGGCAATGCAATCATTTGGAATTAATAGT 312
Db 232 CAAGTAAAGAACTCATTTAATCAAAAATATGCAAGATATGCAAGATTAAGCGCTTTCG 411
Qy 313 AGGCTAATAGTATTTTATGAGGCGAGGCTTGA-----TCCATTTGAGCACTTATGCTT 366
Db 292 CAATTAATGATATTTCTGCTGCTTCAAGGGAAGAAAGATGCAATGGCAATTTTATGGA 351
Qy 367 CTGTGTAAGAGCTTATTAAGAAAAGTATGATCAGGCTGTAAGAAAATGCTCTTGA 426
Db 352 CAAGTAAAGAACTCATTTAATCAAAAATATGCAAGATATGCAAGATTAAGCGCTTTCG 411
Qy 427 GAGCTAAGAGTTTACAGGAAATTAATGAGACTATATCAACTAGACTGCAAGCATGGCTA 486
Db 412 GAATTAAGAGATTTAGTAAATATATACCAATTAATATTAATGCGCTGGAAGATGGAA 471
Qy 487 GTTAAACAAGATGATGCAATCGAGGGCACTAGT---AAGCAGATATGCAATTTGAT 543
Db 472 GAAATATCAATGCTGTCAGAGCTTACAGATGTCGAAATGCAATTTGAAATCTGAT 531
Qy 544 AACTTTTTCGAAAAGATATGCAAAATTTCAAGAAAGAACTTGAATTTATTTGTTA 603
Db 532 AGTTTATTTACGCAATTAATGATGCTTTTATGATGCAAAATTTGAAATGCAATTCCTT 591
Qy 604 CCAATATATGCAACAGCGCGAAATTTGCAATTTATTTATTAAGAGATGCTGATTTT 663
Db 592 ACTGTAATATGCAATGCGACCACTTCAATTTACTGTTATTAAGAGCGGCTCAATTTT 651
Qy 664 GGAGCAAGTGGCAATTAAGTATGATGAAATTCGTATTAATTAATCAGACTACAGAGA 723
Db 652 GGAGAAAGATGGGATGCTCAACCACTACTATTAAATATATATGATGCTCAATGAA 711

QY 724 CTGATTAGAGATATTAAGATTCATTGTATTAACATTCATTAACAGGGTTTAAATCAATTT 783
 DB 712 CTACTGACAGATATTTCTGATCTGCTGTAAAGTGTATGAATCGTTTAAAGCAATTTA 771
 QY 784 AATCGCTCAATATGCTCAAGATGGGTGAGCTTTAATATGTTTCTGTACATATGACATTA 843
 DB 772 AAAGGCACGAGCGCTTAACAATGAGTGTGACTATTAACCAATTCCTGTAGAAATGACACTG 831
 QY 844 ACAGTATTAATCTCGCATATTTATTTCCAACTAGATTCAGCTAGTATTCATTTGCA 903
 DB 832 GCGGTTTAAATGTTGTTCATTAATCCCAATTTATACACAGCAGTACCCCAATGAAA 891
 QY 904 GTAAAAACGAAATGCTAGGAGTTTATACAGATCCAGTAGG 947
 DB 892 ACGAAGCACACTTAACAAGGAAATATATACAGATCCACTGGG 935

RESULT 6

US-10-414-637-15
 ; Sequence 15, Application US/10414637
 ; Publication No. US20030177528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Nicholas B. Duck
 ; APPLICANT: Xiang Feng
 ; APPLICANT: Ronald D. Flannagan
 ; APPLICANT: Theodore W. Kahn
 ; APPLICANT: Lynn E. Sims
 ; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
 ; FILE REFERENCE: 35718/237005
 ; CURRENT APPLICATION NUMBER: US/10/414,637
 ; PRIOR FILING DATE: 2003-04-16
 ; PRIOR APPLICATION NUMBER: US/10/032,717
 ; PRIOR FILING DATE: 2001-10-23
 ; PRIOR APPLICATION NUMBER: 60/242,838
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 2010
 ; TYPE: DNA
 ; ORGANISM: *Bacillus thuringiensis* (truncated)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(2010)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (0)...(0)
 ; OTHER INFORMATION: 1218-1A
 ; US-10-414-637-15

Query Match 11.5%; Score 235.6; DB 6; Length 2010;
 Best Local Similarity 56.5%; Pred. No. 2,4e-43;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAATTAATGATATGAAATGTTGAGTCTTTACGAATCACTTAATATGCTTAAT 72
 DB 10 AATATATCAATGATATGAAATGATATGATGCGACACTTCTA---CTTCTGATCCAAAT 66
 QY 73 TGTATCAAGTATCACTAGCAAAAGATCCCAATATGATATGCGAAACAGAACTAT 132
 DB 67 GATTCTACAGATATCCCTTTTGGCAATGAGCCAAATGCGCTACAAATATGATTTAT 126
 QY 133 AAAGATGCTTAATATGTTGATTCAAATACAAATTTATGTTGATATAGCACTAT 192
 DB 127 AAGATATATTTAAATATGTCGCGGAAATGCTAGTAATACCTGTGTC-----177
 QY 193 TCTAGCCTGAAGCTGTTTAAGTATGAGATGCTGTTTAAAGGATATTAACAGTGA 252
 DB 178 -----CTGTAAATCTTTGTTAGCGGCAAGATGCACTAAGCGCGCAATTTGATATAGTA 231

QY 253 GGAATATATCTTTCGAATTTAAGGGGTCCTTTGGCAAGTCAATCTTTGGAATTAATAGT 312
 DB 232 GGTAAATTAATCTATCAGGTTTAGGGGTCCATTTGTTGGCCGATAGAGTCTTTATATCT 291
 QY 313 AGCTAATAGTATTTTATATGGGAGGGCTGA-----TCCATTTGAGCACTTAATGTT 366
 DB 292 CAATTAATATATTTCTGTGGCCCTTTCAGGGGAAAGATCAATGGGAAATTTTATAGAA 351
 QY 367 CTGTTGAAGAGCTTTATTAAGAAAGATATAGATCAGCGTGTAAAGAAATGCTTAGA 426
 DB 352 CAAGTAAAGAACTCATTAATCAAAAATATGCAAGATATGCAAGAAATTAAGCGCTTTCG 411
 QY 427 GAGCTAAGAGTTTACAGGGAATTAATGAGCTATATCAAACTAGCTCAAGCAATGCTA 486
 DB 412 GAATTAAGAAATAGTATAGTATTAATTAATCAATTAATATCTAATCTGCTGTAAGATGGAA 471
 QY 487 GTTAACAAGATATGACATTCGAGGGCACTAGT--AACGAGTATGCAATTTGTTAT 543
 DB 472 GAAATTCGAATATGTTTCMAAGGCTTACGAGATGCGAAATGATTTGAAATCTGGAT 531
 QY 544 AACTTTTTCGAAAGAAATATGCGCAAAATTCAGAGAAAGAAATTTGAAATTTTATGTTA 603
 DB 532 AGTTTATTAAGCAATATATGCAATCTTTTAGAGTGACAAATTTTGAAGTACATTCCTT 591
 QY 604 CCAGTATATGACAGAGCGGCAATTTGCAATTTAATTTATTAAGATGCTGATATTTT 663
 DB 592 ACTGTATATGCAATATGAGGCAACCTTCATTTCTGTATTAAGAGCGGCTCAATTTT 651
 QY 664 GAGACAGTGGCAATTTAGTATATGAAATTCGTATATTTATATATGACATTAACAAGA 723
 DB 652 GGAAGAAATAGGGGATGCTCAACACTATTAATTAATTAATATATGATATCTCAATGAAA 711
 QY 724 CTGATTAGAGATATTAAGATTCATTGTATTAACATTCATTAACAGGTTTAAATCAATTT 783
 DB 712 CTACTGACAGATATTTCTGATCTGCTGTAAAGTGTATGAATCGTTTAAAGCAATTTA 771
 QY 784 AATCGCTCAATATGCTCAAGATGGGTGAGCTTTAATATGTTTGTACATATGACATTA 843
 DB 772 AAAGGCACGAGCGCTTAACAATGAGTGTGACTATTAACCAATTCGTAGAAATGACACTG 831
 QY 844 ACAGTATTAATCTCGCATATTTATTTCCAACTAGATTCAGCTAGTATTCATTTGCA 903
 DB 832 GCGGTTTAAATGTTGTTCATTAATCCCAATTTATACACAGCAGTACCCCAATGAAA 891
 QY 904 GTAAAAACGAAATGCTAGGAGTTTATACAGATCCAGTAGG 947
 DB 892 ACGAAGCACACTTAACAAGGAAATATATACAGATCCACTGGG 935

RESULT 7

US-10-606-320-11
 ; Sequence 11, Application US/10606320
 ; Publication No. US20040091505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Ronald D. Flannagan
 ; APPLICANT: Rafael Herrmann
 ; APPLICANT: Theodore W. Kahn
 ; APPLICANT: Albert L. Lu
 ; APPLICANT: Billy Fred McCutchen
 ; APPLICANT: James K. Presnall
 ; APPLICANT: Cao-Guo Yu
 ; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
 ; FILE REFERENCE: 35718/263948
 ; CURRENT APPLICATION NUMBER: US/10/606,320
 ; PRIOR FILING DATE: 2003-06-25
 ; PRIOR APPLICATION NUMBER: 60/391,786
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: 60/460,787
 ; PRIOR FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 134

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-10-606-320-11

Query Match 11.5%; Score 235.6; DB 7; Length 2010;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAATPAAATGAAATGAAATGTTGATGCTTTACGAATCACTCTAATATGCTAAT 72
DB 10 AATAATCAAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 66
QY 73 TGTATCAAGATGATCACTAGCAAAAGATCCAAATGACTATGGGAAACAGAACTAT 132
DB 67 GATTTAAGATGATCACTAGCAAAAGATCCAAATGACTATGGGAAATGATGAT 126
QY 133 AAGAATGCTAAATATGCTGATGATCAAAATGAAATGAAATGAAATGAAATGAAAT 192
DB 127 AAGATTAATTTAAATATGCTGCTGGGAAATGCTAGGAAATACCTGTTCA----- 177
QY 193 TCTAGCCCTGAAGCTGCTTAAGTGAACGATGCTGTTTAAAGGATTAACAGTGA 252
DB 178 -----CTGAAATGATCTGTTAGCGGCAAGATGCAAGTCAAGCCCAATGATATAGTA 211
QY 253 GGGACTATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCTTGGAAATTAAT 312
DB 232 GGTAAATTAATCAAGTTTAGGGGTCCTTTCGAATTTAGGGGTCCTTTCGAATTTACT 291
QY 313 AGGCTAATAGTATTTTATGAGGAGGCTGA-----TCCATTTGAAGCACTTATGTT 366
DB 292 CAACCTATTGATATTTCTGTCGCTTCAAGGGAAGAAAGTCAATGGGAAATTTTATGAA 351
QY 367 CTTGTTGAAGATTTTAAAGAAAGTATGATCAGGCTGTAAAGAAATGCTCTTGA 426
DB 352 CAAGTGAAGAACTCAATTAATCAAAAAATGCAAAATATGCAAGAAATGAAGGCTTTG 411
QY 427 GAGCTGAAGGTTTACAGGGAATTTAGAGCTATATCAAACTGACGCAAGATGCTA 486
DB 412 GAATTAAGAGATTTAGGTAATTAATTAATCAATTAATTAATTAATTAATTAATTA 471
QY 487 GTTAAACAAGATGATGACATCGAGGCACTAGT---AAGCAGATATGCAATTTGAT 543
DB 472 GAAATTCGAATGCTTCAAGAGCTTACAGAGATGAGAAATGATTTGAAATCCGGAAT 511
QY 544 AACTTTTGAAGAAAGATATGCCAAATTCAGAGAAAGAACTTTGAAATTTATTTGTTA 603
DB 532 AGTTTATTTACGCAATATATGCAATCTTTTATGAGTGAAGAAATTTGAAGCAATTCCT 591
QY 604 CCAATTAATGCAACAAGCCGGAATTTGCAATTTTATTAAGATGCTGATTAATTT 663
DB 592 ACTGTAATGCAATGCAAGCCGGAATCTTCAATTTTATTAAGAGCGGTCATATTTT 651
QY 664 GGAAGCAGTGCATTTAGGTGATGTAAGAAATCGTATTAATTAATTAATTAATTAAT 723
DB 652 GGAAGAAATGGGATGCTCAACAACATTAATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATTAAGATCAATTTGATTAATTAATTAATTAATTAATTAATTAAT 783
DB 712 CTATAGCAAGAAATATCTGATCACTGCTGTAAGTGAATGAATGCTGTTAGCAAAATTA 771
QY 784 AATCGCTCAAGTCTCAAGATTTGGGTGAGCTTTAATAGGTTTGTACAGATTAAGACATTA 843
DB 772 AAAGGACAGAGCTCAAAACAAATGGGTTGACTAATTAACCAATTCGTAGAGAAATGACACTG 831

QY 844 ACAGATTAATGATCTGCAATTAATTTTCCAAACTATGATCAAGTATGATTCATTAGCA 903
DB 832 GCGGTTTATGATGTTGTCATTAATTTCCAAATTAATGACACGCGCAATGAA 891
QY 904 GTTAAAGCAATTTGCTAGTGAAGTTTATACAGATCCAGTAGG 947
DB 892 ACGAAAGCAACCTAACAGAGGAAATGATTAATGATCACTGAG 935

RESULT 8
US-10-746-914-11

; Sequence 11, Application US/10746914
; Publication No. US20040210963A1
; GENERAL INFORMATION:
; APPLICANT: Albert L. Lu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/268350
; CURRENT APPLICATION NUMBER: US/10/746,914
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-10-746-914-11

Query Match 11.5%; Score 235.6; DB 8; Length 2010;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAATPAAATGAAATGAAATGTTGATGCTTTACGAATCACTCTAATATGCTAAT 72
DB 10 AATAATCAAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 66
QY 73 TGTATCAAGATGATCACTAGCAAAAGATCCAAATGACTATGGGAAACAGAACTAT 132
DB 67 GATTTAAGATGATCACTAGCAAAAGATCCAAATGACTATGGGAAATGATGAT 126
QY 133 AAGAATGCTAAATATGCTGATGATCAAAATGAAATGAAATGAAATGAAATGAAAT 192
DB 127 AAGATTAATTTAAATATGCTGCTGGGAAATGCTAGGAAATACCTGTTCA----- 177
QY 193 TCTAGCCCTGAAGCTGCTTTAAGTGAACGATGCTGTTTAAAGGATTAACAGTGA 252
DB 178 -----CTGAAATGATCTGTTAGCGGCAAGATGCAAGTCAATCTTGGAAATTAAT 231
QY 253 GGGACTATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCTTGGAAATTAAT 312
DB 232 GGTAAATTAATCAAGTTTAGGGGTCCTTTCGAATTTAGGGGTCCTTTCGAATTTACT 291
QY 313 AGGCTAATAGTATTTTATGAGGAGGCTGA-----TCCATTTGAAGCACTTATGTT 366
DB 292 CAACCTATTGATATTTCTGTCGCTTCAAGGGAAGAAAGTCAATGGGAAATTTTATGAA 351
QY 367 CTTGTTGAAGATTTTAAAGAAAGTATGATCAGGCTGTAAAGAAATGCTCTTGA 426
DB 352 CAAGTGAAGAACTCAATTAATCAAAAAATGCAAAATATGCAAGAAATGAAGGCTTTG 411


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QY 133 AAGAAATGCTAAATATGTGATTCAAATACACAATTTATGCTGATATAGACGCTAT 192
D 127 AAGATTAATTTAAAAATGTGGGGGAAATGCTAGTAATACCTGTTCA----- 177
QY 193 TCTAGCCCTGAAGCTCTTTAAGTACAGAGATGCTGTTTAAACGGGTATTAACAAGTGA 252
D 178 -----CCTGAAGTACTGTTAGCGGCAAGATGCACATAAGCCGCAATGATATATGTA 231
QY 253 GGGACTATCTTCTGAAATTAAGGGGTCCTTTGSCAGTCAATATTTGGAATTAATAGT 312
D 232 GGTAAATTAATCAATAGGTTTAGGGGTCCTCATTTGTTGGCCGATATGAGTCTTAACT 291
QY 313 AGGCTAATAGGTAATTTATGCGGAGGCTGTA-----TCCATTTGAAGCACTTATGTT 366
D 292 CAATTAATGATATCTGTGGCCCTTCAAGGGGAAAGATGCAATGGGAAATTTTATATGAA 351
QY 367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCGTGAAGAAAATGCTCTTGA 426
D 352 CAAGTAAAGAACTCAATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCCCTTGC 411
QY 427 GAGCTAAGAGTTTACAGGGAATATAGACTATATCAATCACTGCAAGCAATGGCTA 486
D 412 GAATTAAGAAAGATTAAGGTAATTAATTAATCAATTAATCACTGCTTGAAGATGGAA 471
QY 487 GTTAAACAAGATGATGACAAATCGAGGGCACTAGT---AAGCAGTATGCAATTTGAT 543
D 472 GAAATTCAAATGTTTCAAGAGCTTACAGAGATGCGAAATGCAATTTGAAATCTTGAT 531
QY 544 AACTTTTTCGAAAAGAAATATGCCAAAATTCAGAGAAAAGAACTTTGAATTTTATGTTA 603
D 532 AGTTATTTTACGCAATATATATGCGCATCTTTAGATGACAAATTTGAAGTACATTCCT 591
QY 604 CCAATATATCAACAAGCCCGGAATTTGCAATTTATTTATTAAGATGCTGATATTTT 663
D 592 ACTGTAATCAATGCAAGCCCAACCTTCATTTACGTTATTTAAAGAGCGGTCAATTTT 651
QY 664 GAGACAGTGGCAATTAAGGTATGATGAATTCGTATTAATTAATCACTCAAGCA 723
D 652 GGAAGAAATGCGGATGCTCAACAACCTATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATTAAGATTCATTTGATTAACAATTCATTAACAAGGTTTAAATCAATTT 783
D 712 CTTACTGCAAAATTTCTGATCACTGTGTAAGTGTATGAACTGTTTAGCAAAATTA 771
QY 784 AATCGCTCAATGCTCAAGATGCGTGAAGCTTTAATAGTTTGTATCAAGATATGACTTA 843
D 772 AAGGCGACGAGCGCTAAACAATGGGTTGACTATTAACAATTCCTAGAGAAATGACACTG 831
QY 844 ACAGTATTAATCTCGCAATATTAATTCAAACATATGATCAAGTATGATATTCATTGCA 903
D 832 GCGGTTTAATGTTGTTGCTATTAATTCCAAAATTAATTAACAACGCACTTACCAATGAA 891
QY 904 GTAAAAACGGAATTAAGTGAAGATTTATATACAGATCCAGTAGG 947
D 892 ACGAAAGCAACAATTAACAAGGAAATATATACGATCCACTGGG 995

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RESULT 12
US-10-746-914-1
; Sequence 1, Application US/10746914
; Publication No. US20040210963A1
; GENERAL INFORMATION:
; APPLICANT: Albert L. Lu
; TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/268350
; CURRENT APPLICATION NUMBER: US/10/746,914
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04

```

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; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12Ib-1
US-10-746-914-1

```

Query Match 11.5%; Score 235.6; DB 8; Length 3621;

Best Local Similarity 56.5%; Pred. No. 3.1e-43;

Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

QY 13 AAAAAATTAATGAATTAATGTAATGTTGAGTCTTTCAGATCAATCTAATATGCTAAT 72
D 10 AATTAATCAAAATGAATTAATGAATTAATGATGCAACCTTCTA---CTTGTATCAAT 66
QY 73 TGTATCAAGTATCCACAGCAAAAAGATCCCAAAATGACTATGCGAAACAGAACTAT 132
D 67 GATTTCAAGATATACCTTTTGGCAATGAGCCCAAAATGCGTACAAAATATGATAT 126
QY 133 AAGAAATGCTAAATATGTTGATTCAAATTAACAATTTATGTTGATATAGCAGCTAT 192
D 127 AAGATTAATTTAAAAATGCTGCGGGAATGCTAGTAATACCTGTTCA----- 177
QY 193 TCTAGCCCTGAAGCTCTTTAAGTACAGAGATGCTGTTTAAACGGGTATTAACAAGTGA 252
D 178 -----CCTGAAGTACTGTTAGCGGCAAGATGCACATAAGCCGCAATGATATATGTA 231
QY 253 GGGACTATCTTCTGAAATTAAGGGGTCCTTTGSCAGTCAATATTTGGAATTAATAGT 312
D 232 GGTAAATTAATCAATAGGTTTAGGGGTCCTCATTTGTTGGCCGATATGAGTCTTAACT 291
QY 313 AGGCTAATAGGTAATTTATGCGGAGGCTGTA-----TCCATTTGAAGCACTTATGTT 366
D 292 CAATTAATGATATCTGTGGCCCTTCAAGGGGAAAGATGCAATTTGAAATCTTGAT 531
QY 367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCGTGAAGAAAATGCTCTTGA 426
D 352 CAAGTAAAGAACTCAATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTGC 411
QY 427 GAGCTAAGAGTTTACAGGGAATTAAGACTATATCAAACTGACATGCAAGCATGGCTA 486
D 412 GAATTAAGAAAGATTAAGTAAATTAATTAATCAATTAATTAATTAATTAATTAATTA 471
QY 487 GTTAAACAAGATGATGACAAATCGAGGGCACTAGT---AAGCAGTATGCAATTTGAT 543
D 472 GAAATTCAAATGTTTCAAGAGCTTACAGAGATGCGAAATGCAATTTGAAATCTTGAT 531
QY 544 AACTTTTTCGAAAAGAAATATGCCAAAATTCAGAGAAAAGAACTTTGAATTTTATGTTA 603
D 532 AGTTATTTTACGCAATATATATGCGCATCTTTAGATGACAAATTTGAAAGTACATTCCT 591
QY 604 CCAATATATCAACAAGCCCGGAATTTGCAATTTATTTATTAAGATGCTGATATTTT 663
D 592 ACTGTAATCAATGCAAGCCCAACCTTCATTTACGTTATTTAAAGAGCGGTCAATTTT 651
QY 664 GAGACAGTGGCAATTAAGGTATGATGAATTCGTATTAATTAATTAATTAATTAATTA 723
D 652 GGAAGAAATGCGGATGCTCAACAACCTATTAATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATTAAGATTCATTTGATTAACAATTCATTAACAAGGTTTAAATCAATTT 783
D 712 CTTACTGCAAAATTTCTGATCACTGTGTAAGTGTATGAACTGTTTAGCAAAATTA 771

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QY 784 AATCGCTCAATGCTCAAGTGTGGAGCTTTAATAGCTTTCGTCACATATGACATTA 843
DB 772 AAAGGACGCGCGCTAAACATGAGTGTGATATACCAATTCGTTAGAGAAATGACACTG 831
QY 844 ACAGTTTATGATCTCGCAATATATTTCCAACTATGATCCAGTGTGATTCATTAAGCA 903
DB 832 GCGGTTTATGATGTGTGATATATTCGCAATATATGACACGACGTAACCAATGGAA 891
QY 904 GTAAAAACGGAATTGACTAGGGAAGTTTATATACATCCAGTACG 947
DB 892 ACGAAGGACACACTAACAGGAAGTATATACAGATCCACTGGG 935

RESULT 13

US-11-021-115-5
; Sequence 5, Application US/11021115
; Publication No. US20050166284A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Flannagan, Ronald D.
; APPLICANT: Hermann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Bill F.
; APPLICANT: Presnall, James K.
; APPLICANT: Rice, Janet A.
; APPLICANT: Wong, James F.
; APPLICANT: Yu, Cao-Guo
; TITLE OF INVENTION: Plant Activation of Insect Toxin
; FILE REFERENCE: 035718/285836
; CURRENT APPLICATION NUMBER: US/11/021,115
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 60/532,185
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis*
US-11-021-115-5

Query Match 11.5%; Score 235.6; DB 10; Length 3621;
Best Local Similarity 56.5%; Pred. No. 3.1e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
QY 13 AAAAAATAAATGAATGAAATGTTGATCTTTACGATCAACTTAATATGCTTAAT 72
DB 10 AATATCAAAATGAAATGAAATGATGATGACACCTTCTA---CTTGTATCCAT 66
QY 73 TGTATCCAAAGTATCCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
DB 67 GATTTCACAGATACCTTTTGGCAATGACCAAAATCGCTACAAATATGATATAT 126
QY 133 AAGAAATGGTAATATGTGTGATCAAAATACAACTATTTGTGATATACAGATAT 192
DB 127 AAGATATATTTAAAAATGCTGGGAAAGCTAGTGAATACCTGGTTCA----- 177
QY 193 TTAGCCCTGAGCTGCTTAAGTATGATGATGCTGTTTAAAGGATATTAAGATTA 252
DB 178 -----CTGAAATACCTTTGATGCGAAGATGCTAAAGCCGCAATTTGATATAGTA 231
QY 253 GGGACTATATCTTTCGAATTTAGGGGCTCCCTTTGGCAAGTCAATCATTGGAAATTAAT 312
DB 232 GGTAAATTAATCAAGTTTAGGGGCTCCATTTGTTGGCGCATGATGATCTTTATACT 291
QY 313 AGGCTAATAGATATTTTATGGGCAAGGCTCTGA-----TCATTTGAAGCACTTAATGTT 366
DB 292 CAATTAATGATATTTCTGTGCTTCAGGGGAAAGAGTCAATGGAAATTTTATAGTA 351
QY 367 CTGTTGAGAGGCTTTTAAAGAAAGATATGATCAGGCTTAAGAGAAATGCTCTTAA 426
DB 352 CAAGTAAAGAACTCATTTATCAAAAAATAGCAATATGCAAGAAATTAAGCGCTTTG 411

QY 427 GAGCTTGAAGGTTTACAGGAAATTTATGACATATATCAAACTATGATGCAAGATGGCTTA 486
DB 412 GAATTAAGAAAGATTTAGTATATATTAACAAATATATCTAATCTGCGCTTGAAGAAATGGAA 471
QY 487 GTTAACAAAGATGATGACAAATGAGAGGCACTAGT---AAGCGATGCAATTTGTTGAT 543
DB 472 GAAATTCGAATGTTTCAAGAGGCTTTACAGATGTGCGAAATGATTTGAAATCTCGAT 531
QY 544 AACTTTTGGAAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTTA 603
DB 532 AGTTTATTTACGCAATATATATGCACTTTTAAAGTACAAATTTTGAAGTACATTCCTT 591
QY 604 CCAATATATGACAAAGCCCGCAATTTGCAATTTTATTTTAAAGATGCTGATATTTT 663
DB 592 ACTGATATGATGATGACAGCCCAACTTCACTTTTAAAGGACGCTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTATGATGATGAAATTCGATATTTATATATACAGACTACAGGA 723
DB 652 GAGAAAGATGGGATGTGCAACACTATTTATATCAATTTATGATGTCAAATGAAA 711
QY 724 CTGATTAAGAAATATTAAGATCATTTGATATACATTTCTATACCGAGGTTTAAATCAATTT 783
DB 712 CTACTGAGAAATATTTCTGATCAGTGTGTAAGTGTATGAAACTGTTTACGAAATTA 771
QY 784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTAATAGGTTTGTACAGATATGACATTA 843
DB 772 AAAGGACGACGCTTAACAAATGAGTGTGACTATACAAATTCGTAAGAAATGACACTG 831
QY 844 ACAGTATGATCTGCAATATTTATTTCCAACTATGATGACAGTGTGATCCATTAAGCA 903
DB 832 GCGGTTTATGATGTGTGATATATTCGCAATATATGACACGACGTAACCAATGGAA 891
QY 904 GTAAAAACGGAATTGACTAGGGAAGTTTATATACATCCAGTACG 947
DB 892 ACGAAGGACACACTAACAGGAAGTATATACAGATCCACTGGG 935

RESULT 14

US-10-032-717-27
; Sequence 27, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins with
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: *Bacillus thuringiensis*
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-10-032-717-27

Query Match 11.5%; Score 235.6; DB 5; Length 4874;
Best Local Similarity 56.5%; Pred. No. 3.6e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
QY 13 AAAAAATAAATGAATGAAATGTTGATGCTTTACGATCAACTTAATATGCTTAAT 72

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Db      740 AATATCAAAATGATATGAAATATATAGATGCAACCTTCTA---CTTCTGATCCAAAT 796
Qy      73 TGTATCAAGATATCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db      797 GATTCTACAGATACCTTTTGGCAATGACCAAAATGCGTACAAAATATGATAT 856
Qy      133 AAGAAATGCTAAATATGATGATTCAAATACAAATTTATGATATATAGACGAT 192
Db      857 AAGATATTTAAATATGTCGGCGAAATGCTAGATATACCTGTTCA----- 907
Qy      193 TCTAGCCCTGAGAGCTGTTTATGATGACAGATGCTGTTTAAAGGATATTAACAGTGA 252
Db      908 -----CTGAAAGACTTGTATGAGCGCAAGATGCACTAAGCGCGCAATGATATGTA 961
Qy      253 GGGACTATACCTTTCGAATTTAGGGGCTCCCTTGGCAAGTCAATCATTTGAAATATAGT 312
Db      962 GGTAAATTTACTATACGTTTATGAGGCTCCATTTGTTGGCGATGATGATCTTTATATCT 1021
Qy      313 AGGCTAATAGTATTTTATGCGGAGGCTGA-----TCCATTTGAAGCACTTATGTT 366
Db      1022 CACTTATGATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGAA 1081
Qy      367 CTGTGTAAGAGCTTATTAAGAAAGATATGATCAGCGTTTAAAGAAATGCTTTAGA 426
Db      1082 CAATGTAAGAACTCATTAATCAAAAATATGCAAGATATGCAAGATTAAGCGCTTTCG 1141
Qy      427 GACTTGAAGGTTTACAGGGAATTAATGAGACTATATCAACTAGACTGCAAGATGCTGA 486
Db      1142 GAATTTGAAGATTAAGGTAATTAATTAATCAATTAATCTAATCTGCGCTTGAAGATGGA 1201
Qy      487 GTTAAACAGATATGATCAATCGAGGCACTAGT---AAGCGATATGCAATTTGTTAGT 543
Db      1202 GAAATTCAAATGTTTCAAGAGCTTACAGATATGCGAAATGCAATTTGAATTCCTGAT 1261
Qy      544 AACTTTTGAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAATTTTATGTTA 603
Db      1262 AGTTATTTACGCAATATATGCACTTTTATGAGTGAAGATTTGAAGTACATTCCTT 1321
Qy      604 CCAATATATGCAAGAGCGGGAATTTGCAATTTATTTATTAAGATGCTGATATTTT 663
Db      1322 ACTGTAATGCAATGCGAGCAACCTTCAATTTACTGTTATTAAGAGCGGCTCAATTTT 1381
Qy      664 GGAGCAAGTGGCAATTAGGTGATGATGAATTCGTAATTTATTAATCACTACAGGA 723
Db      1382 GGAGAAAGATGGGATGCTCAACAACATCTATTAATTAATCTATGATTCGTAATGAAA 1441
Qy      724 CTGATTAAGAAATATTAAGATTCATTTGTAACAATTTCTATAACAAGGCTTTAAATCAATTT 783
Db      1442 CTTACTGCAAGATATTTCTGATCTAGTGAAGGTATGAAACTGGTTTACCAAAATTA 1501
Qy      784 AATCGCTCAAAATGCTCAAGATTTGGGTAGCTTTATATAGTTTGGTACAGATATGACCTTA 843
Db      1502 AAGGCAAGCGGCTTAACAATGGGTAGCTATTAACAATTTCCGTAAAGAAATGACCTG 1561
Qy      844 ACAGATTAATGATCTCGCAATATTAATTCAAACTATGATCCAGTAGATTTCACTTGA 903
Db      1562 GCGGTTTATGATGTTGTTGATTTATTCCAAAATTAATACACGCACTACCAATGGA 1621
Qy      904 GTTAAACGGAATGACTAGGGAAGTTTATACAGATCCAGTAGG 947
Db      1622 ACGAAGCAACAATTAACAAGGAAGTATATACAGATCCACTGGG 1665

```

RESULT 15
US-10-414-637-27

; Sequence 27, Application US/10414637
; Publication No. US2003017528A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Nicholas B. Duck

; APPLICANT: Xiang Feng

; APPLICANT: Ronald D. Flanagan

; APPLICANT: Theodore W. Kahn

```

; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Gene Encoding No. US2003017528A1e1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-10-414-637-27

```

Query Match 11.5%; Score 235.6; DB 6; Length 4874;
Best Local Similarity 56.5%; Pred. No. 3,6e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

Qy      13 AAAAAATAAATGAATATGAAATGTTGATGCTTTTCGAATCAACTAATATATGCTTAAT 72
Db      740 AATATCAAAATGATATGAAATATATAGATGCAACCTTCTA---CTTCTGATCCAAAT 796
Qy      73 TGTATCAAGATATCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db      797 GATTCTACAGATACCTTTTGGCAATGACCAAAATGCGTACAAAATATGATAT 856
Qy      133 AAGAAATGCTAAATATGATGATTCAAATACAAATTTATGATATATAGACGAT 192
Db      857 AAGATATTTAAATATGTCGGCGAAATGCTAGATATACCTGTTCA----- 907
Qy      193 TCTAGCCCTGAGAGCTGTTTATGATGACAGATGCTGTTTAAAGGATATTAACAGTGA 252
Db      908 -----CTGAAAGACTTGTATGAGCGCAAGATGCACTAAGCGCGCAATGATATGTA 961
Qy      253 GGGACTATACCTTTCGAATTTAGGGGCTCCCTTGGCAAGTCAATCATTTGAAATATAGT 312
Db      962 GGTAAATTTACTATACGTTTATGAGGCTCCATTTGTTGGCGATGATGATCTTTATATCT 1021
Qy      313 AGGCTAATAGTATTTTATGCGGAGGCTGA-----TCCATTTGAAGCACTTATGTT 366
Db      1022 CACTTATGATATTTCTGTGGCTTCAGGGGAAAGATGCAAGATTTTATGGA 1081
Qy      367 CTGTGTAAGAGCTTATTAAGAAAGATATGATCAGCGGTATGAGAAATGCTTTAGA 426
Db      1082 CAATGTAAGAACTCATTAATCAAAAATGCAAGATATGCAAGATTAAGCGCTTTCG 1141
Qy      427 GACTTGAAGGTTTACAGGGAATTAATGAGACTATTAACAACCTAGCTGCAAGAGGCTGA 486
Db      1142 GAATTTGAAGATTAAGTATATTAATTAACAATTTATCTAATCTGCGCTGAAGATGGA 1201
Qy      487 GTTAAACAGATATGCAATTCGAGGCACTAGT---AAGCGATATGCAATTTGTTAGT 543
Db      1202 GAAATTCCAAAATGTTTCAAGAGCTTACAGATATGCAAGATTAAGATTTGAAATTCCTG 1261
Qy      544 AACTTTTGAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
Db      1262 AGTTATTTACGCAATATATGCACTTTTATGAGTGAAGATTTGAAGTACATTCCTT 1321
Qy      604 CCAATATATGCAAGAGCGGGAATTTGCAATTTATTTATTAAGATGCTGATATTTT 663
Db      1322 ACTGTAATGCAATGCGAGCAACCTTCAATTTACTGTTATTAAGAGCGGCTCAATTTT 1381
Qy      664 GGAGCAAGTGGCAATTAGGTGATGATGAATTCGTAATTTATTAATCACTACAGGA 723
Db      1382 GGAGAAAGATGGGATGCTCAACAACATCTATTAATTAATGATGCTCAAAATGAAA 1441

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